

STIC-Biotech/ChemLib

84063

From: Chan, Christina
Sent: Monday, January 13, 2003 7:59 AM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE:

RECEIVED

JAN 13 2003

STIC-BIOTECH/CHEM LIB
(STIC)

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Minnifield, Nita
Sent: Sunday, January 12, 2003 1:12 PM
To: Chan, Christina
Subject:

Christina,
Please approve, 2 month amdt.

STIC

09/144886

PALM indicates "NO BIOTECH DATA"; however application file has a RSL copy with "ENTERED" stamped on it. Date on RSL is 9/1/99

Please do a commercial sequence search on SEQ ID NO:63 and 87 of the above application. Please provide a paper copy of the results.

Thanks,

Nita M. Minnifield

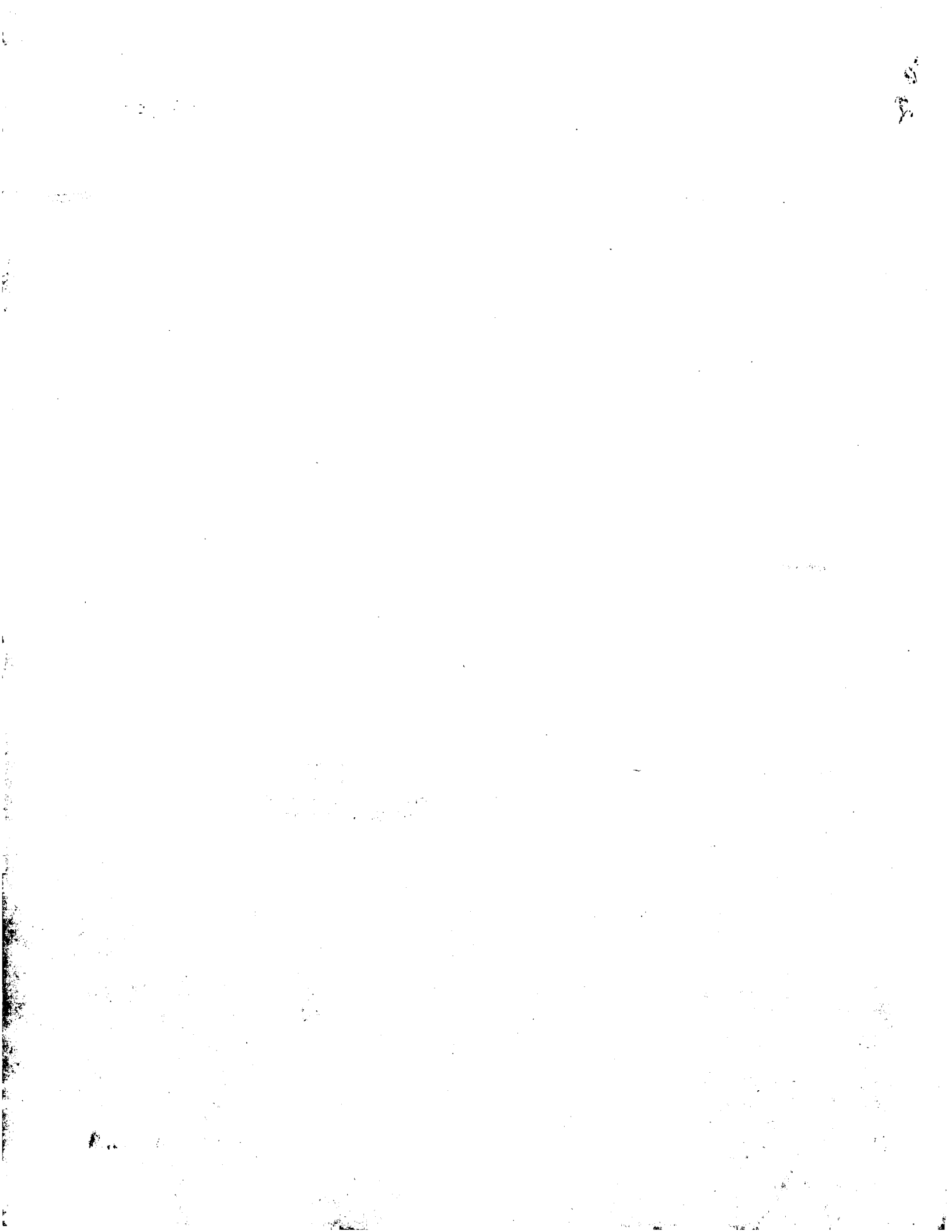
Art Unit 1645
Office CM1-8A07
Mailbox CM1-8E12
703-305-3394

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: Bob
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 1-13-03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:10:24 : Search time 14.3652 Seconds
(without alignments)
789.676 Million cell updates/sec

Title: US-09-144-886-63

Perfect score: 633

Sequence: 1 QVQLDSGGGLVPRGSLKLT.....YRVDAMDYWGQGTITVYSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575.5	90.9	152	B26471	Ig heavy chain pre
2	547.5	86.5	122	E27888	Ig heavy chain v r
3	545.5	86.2	120	S55536	Ig heavy chain v r
4	544	85.9	119	D27889	Ig heavy chain v r
5	538.5	85.1	120	S55537	Ig heavy chain v r
6	538	85.0	119	B27889	Ig heavy chain v r
7	534.5	84.4	120	S55539	Ig heavy chain v r
8	533	84.2	119	E27888	Ig heavy chain v r
9	523.5	82.7	120	S55538	Ig heavy chain v r
10	517.5	81.8	118	E27889	Ig heavy chain v r
11	515	81.4	121	I27887	Ig heavy chain v r
12	510	80.6	121	S55540	Ig heavy chain v r
13	508	80.3	98	HYMS96	Ig heavy chain v r
14	506.5	80.0	119	A43413	Ig heavy chain v r
15	506	79.9	121	H27888	Ig heavy chain v r
16	502.5	79.4	138	S09258	Ig heavy chain v r
17	502	79.3	118	PH0096	Ig heavy chain v r
18	502	79.3	254	B31790	Ig heavy chain v r
19	497	78.5	118	PH0097	Ig heavy chain v r
20	495.5	78.3	118	S20641	Ig heavy chain v r
21	491	77.6	121	A27888	Ig heavy chain v r
22	491	77.6	139	S38808	Ig heavy chain v r
23	490	77.4	121	B27888	Ig heavy chain v r
24	490	77.4	121	H27887	Ig heavy chain v r
25	489	77.3	123	G27888	Ig heavy chain v r
26	487.5	77.0	124	C27888	Ig heavy chain v r
27	487	76.9	101	C27889	Ig heavy chain v r
28	484	76.5	548	S38864	Ig epsilon chain C
29	483.5	76.4	124	I27888	Ig heavy chain v r

30	483	76.3	121	2	D27888	Ig heavy chain v r
31	480.5	75.9	119	2	B34353	anti-peptide Fab'
32	477	75.4	108	2	PL0248	Ig heavy chain v r
33	477	75.4	112	2	A27889	Ig heavy chain v r
34	477	75.4	118	2	S31105	Ig heavy chain (su
35	476	75.2	123	2	S63597	Ig heavy chain, v
36	475.5	75.1	114	2	PH0098	Ig heavy chain v r
37	472	74.6	113	2	S02717	Ig heavy chain v r
38	470	74.2	113	2	S26468	Ig heavy chain v r
39	469	74.1	112	2	S26327	Ig heavy chain v r
40	467	73.8	118	2	PH0095	Ig kappa chain v r
41	465	73.5	108	2	PH1011	Ig heavy chain v r
42	464	73.3	114	2	S31120	Ig heavy chain - h
43	464	73.3	120	2	S12953	Ig heavy chain v r
44	463.5	73.2	117	2	PL0249	Ig heavy chain v r
45	463	73.1	128	2	PH0094	Ig heavy chain v r

ALIGNMENTS

```

RESULT 1
B26471
Ig heavy chain precursor V region (MAK33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C:Accession: B26471; S70410
R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
A:Reference number: A91572; MUID:87248058; PMID:3110009
A:Accession: B26471
A:Molecule type: mRNA
A:Residues: 1-152 <BUC>
A:Cross-references: GB:M16163; NID:9195405; PIDN:AAA38292.1; PID:9195406
R:Lepecque, S.G.; Gearhart, P.J.
J. Exp. Med. 172, 1717-1727, 1990
A:Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' bound
A:Reference number: S70410; MUID:91079775; PMID:2258702
A:Accession: S70410
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-19 <LEB>
A:Cross-references: EMBL:X53776; NID:952475; PIDN:CAA37792.1; PID:952476
C:Genetics:
A:Introns: 16/1
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-152/Product: Ig heavy chain V region MAK33 #status predicted <MAT>
F:34-117/Domain: Immunoglobulin homology <IMB>

Query Match          90.9%; Score 575.5; DB 2; Length 152;
Best Local Similarity 89.4%; Pred. No. 4.3e-44;
Matches 110; Conservative 4; Mismatches 4; Indels 5; Gaps 1;

QY 1 QVQLDSGGGLVPRGSLKLTSCAASGFTSDYIMRWVOTPEKRLKLVATIDSGSYTY 60
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 20 EVQGESGGGLVPRGSLKLTSCAASGFTSDYIMRWVOTPEKRLKLVATIDSGSYTY 79

QY 61 PSVKGKFTISRDNAKNNLYLQMSSILKSEDTAMVYCSR-----YDDAMDYWGQGTITV 115
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80 PSVKGKFTISRDNAKNNLYLQMSSILKSEDTAMVYCARKAYGNGDAMDYWGQGTITV 139
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 116 VSS 118
      |||
DB 140 VSS 142

RESULT 2
E27888
Ig heavy chain V region (H35-C6) - mouse
C:Species: Mus musculus (house mouse)

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A>Note: this sequence was determined from the germine gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 85.0%; Score 538; DB 2; Length 119;
Best Local Similarity 87.4%; Pred. No. 7e-41;
Matches 104; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

Qy 1 OVLOESGGGLVPGGSLKSCAASGFTFSDYMWVWVROTPEKRLMVAATISDGSSTYYP 60
Db 1 EVQLVESGGGLVPGGSLKSCAASGITFSDYTWVWVROTPEKRLMVAATISDGSSTYYP 60
Qy 61 DSVKGRFTISRDNKNNLYLQMSSLSKSEDTAMYYCSRRYD--YDDAMDYWGQGTIVTVSS 117
Db 61 DSVKGRFTISRDNKNNLYLQMSSLSKSEDTAMYYCVRVARDGVFDYWGQGTIVTVSS 119

RESULT 7

S55539
Ig heavy chain V region pe24 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:Accession: S55539

R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
utations in the variable region genes.
A:Reference number: S55528; MUID:95239763; PMID:7536850

A:Accession: S55539

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <BOB>

A:Cross-references: EMBL:X82593; NID:9854312; PIDN:CA57929.1; PID:9854313

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:14-97/Domain: Immunoglobulin homology <IMM>

Query Match 84.4%; Score 534.5; DB 2; Length 120;

Best Local Similarity 86.7%; Pred. No. 1.4e-40;

Matches 104; Conservative 2; Mismatches 11; Indels 3; Gaps 1;

Qy 2 VOLOESGGGLVPGGSLKSCAASGFTFSDYMWVWVROTPEKRLMVAATISDGSSTYYP 61
Db 1 VOLOESGGGLVPGGSLKSCAASGFTFSSYMSVWVROTPEKRLMVAATISDGSSTYYP 60
Qy 62 DSVKGRFTISRDNKNNLYLQMSSLSKSEDTAMYYCSRRYD--DAMDYWGQGTIVTVSS 118
Db 61 DSVKGRFTISRDNKNNLYLQMSSLSKSEDTAMYYCVRVARDGVFDYWGQGTIVTVSS 120

RESULT 8

E27889

Ig heavy chain V region (H158-89H4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: E27888

R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a c

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: E27888

A:Molecule type: DNA

A:Residues: 1-119 <CAT>

A:Experimental source: strain Balb/c

C:Comment: This sequence was determined from the germine gene

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 84.2%; Score 533; DB 2; Length 119;

Best Local Similarity 88.1%; Pred. No. 1.9e-40;
Matches 104; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

Qy 2 VOLOESGGGLVPGGSLKSCAASGFTFSDYMWVWVROTPEKRLMVAATISDGSSTYYP 61
Db 2 VKLVESGGGLVPGGSLKSCAASGFTFSSYMSVWVROTPEKRLMVAATISDGSSTYYP 61
Qy 62 DSVKGRFTISRDNKNNLYLQMSSLSKSEDTAMYYCSRRR--YDDAMDYWGQGTIVTVSS 117
Db 62 DSVKGRFTISRDNKNNLYLQMSSLSKSEDTAMYYCVRGRTYDYAMDYWGQGTIVTVSS 119

RESULT 9

S55538

Ig heavy chain V region pe22 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C:Accession: S55538

R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies u
utations in the variable region genes.
A:Reference number: S55528; MUID:95239763; PMID:7536850

A:Accession: S55538

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <BOB>

A:Cross-references: EMBL:X82591; NID:9854308; PIDN:CA57927.1; PID:9854309

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:14-97/Domain: Immunoglobulin homology <IMM>

Query Match 82.7%; Score 523.5; DB 2; Length 120;

Best Local Similarity 84.2%; Pred. No. 1.4e-39;

Matches 101; Conservative 5; Mismatches 11; Indels 3; Gaps 1;

Qy 2 VOLOESGGGLVPGGSLKSCAASGFTFSDYMWVWVROTPEKRLMVAATISDGSSTYYP 61
Db 1 VKLOESGGGLVPGGSLKSCAASGFTFSSYMSVWVROTPEKRLMVAATISDGSSTYYP 60
Qy 62 DSVKGRFTISRDNKNNLYLQMSSLSKSEDTAMYYCSRRYD--DAMDYWGQGTIVTVSS 118
Db 61 DSVKGRFTISRDNKNNLYLQMSSLSKSEDTAMYYCVRVARDGVFDYWGQGTIVTVSS 120

RESULT 10

E27889

Ig heavy chain V region (H18-S415) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: E27889

R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: E27889

A:Molecule type: DNA

A:Residues: 1-118 <CAT>

A:Experimental source: strain Balb/c

C:Comment: This sequence was determined from the germine gene

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:15-97/Domain: Immunoglobulin homology <IMM>

Query Match 81.8%; Score 517.5; DB 2; Length 118;

Best Local Similarity 84.0%; Pred. No. 4.6e-39;

Matches 100; Conservative 7; Mismatches 9; Indels 3; Gaps 2;

Qy 1 OVLOESGGGLVPGGSLKSCAASGFTFSDYMWVWVROTPEKRLMVAATISDGSSTYYP 60
Db 1 EVQLVDFGGGLVPGGSLKSCAASGITFSDYMWVWVROTPEKRLMVAATITDINTYTY 60

H27888
 Ig heavy chain V region (H37-40) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
 C:Accession: H27888
 R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
 EMBO J. 5, 1577-1587, 1986
 A:Title: Structural and functional implications of a restricted antibody response to a d
 A:Reference number: A91043; MUID:86300656; PMID:2427335
 A:Accession: H27888
 A:Molecule type: DNA
 A:Residues: 1-121 <CAT>
 A:Experimental source: strain Balb/c
 A:Note: This sequence was determined from the germline gene
 C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; Immunoglobulin
 F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 79.9%; Score 506; DB 2; Length 121;
 Best Local Similarity 80.2%; Pred. No. 4.9e-38;
 Matches 97; Conservative 7; Mismatches 13; Indels 4; Gaps 1;

QY 1 QVQLQESGGGLVQPGGSLKLSCAASGFTFSDFYMWVWVROTPPEKRLFWVATISDGSSTYY 60
 :||| |||||:|||| ||||| ||||| | ||||:||||| ||||| |||||
 Db 1 EVQLVESGGGLVQPGGSLNLSCAASGFTFSFYSMSWVRSPEKRLFWVAEISGGSSTYY 60
 QY 61 PDSYKGRFTISRDNKNNLYLQMSSLSKSEDTAMYCSR---YRYDAMDYWGQGTIVTV 116
 ||: ||||| ||||| ||||| ||||| ||||| | ||||| ||||| |||||
 Db 61 PDYVGRFTISRDNKNTLYLQMSLSKSEDTAMYCARREGYGGSSDAMDYWGQGTIVTV 120
 QY 117 S 117
 |
 Db 121 S 121

Search completed: January 13, 2003, 15:13:12
 Job time : 15.3652 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:11:24 ; Search time 8.2087 Seconds
(without alignments) 278.890 Million cell updates/sec

Title: US-09-144-886-63
Perfect score: 633
Sequence: 1 QVQLQESGGGLVFRGGSGLK.....YRVDAMDYWGCGTTVYSS 118

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCRT_NEM_PUB pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB pep:*
4: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCRT_PUBCOMB pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCRT_PUBCOMB pep:*
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9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
10: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
12: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	633	100.0	118	9	US-09-144-886-63
2	597	94.3	118	9	US-09-144-886-63
3	522	84.5	118	9	US-09-144-886-65
4	519	84.0	118	9	US-09-144-886-63
5	518	81.9	144	10	US-09-881-823-12
6	511	80.8	123	9	US-09-144-886-60
7	507	80.2	140	10	US-09-286-240-4
8	504	79.6	118	9	US-09-144-886-67
9	503	79.5	118	9	US-09-144-886-66
10	501	79.1	118	9	US-09-423-800-46
11	501	79.1	137	9	US-09-423-800-76
12	493.5	78.0	140	12	US-10-006-773-4
13	484.5	75.1	269	12	US-10-027-770-5
14	475.5	75.1	269	12	US-10-027-770-2
15	474	74.9	120	10	US-08-229-200A-6
16	473	74.7	443	10	US-09-917-410-4
17	472.5	74.6	119	10	US-09-736-371B-17
18	472.5	74.6	119	12	US-10-060-714-17
19	469	74.1	118	9	US-09-423-800-56

20	469	74.1	137	9	US-09-423-800-77	Sequence 77, Appl
21	468.5	74.0	123	9	US-09-144-886-61	Sequence 61, Appl
22	466.5	73.7	245	9	US-09-956-086-5	Sequence 5, Appl
23	466.5	73.7	245	9	US-09-956-087-5	Sequence 5, Appl
24	466	73.6	98	10	US-09-840-459-39	Sequence 39, Appl
25	465.5	73.5	265	9	US-09-985-442-5	Sequence 5, Appl
26	465.5	73.5	265	10	US-09-983-580-5	Sequence 5, Appl
27	464	73.3	98	10	US-09-840-459-38	Sequence 38, Appl
28	462	73.0	98	10	US-09-840-459-45	Sequence 45, Appl
29	460.5	72.7	117	8	US-08-790-540A-6	Sequence 6, Appl
30	460.5	72.7	117	8	US-08-791-391A-6	Sequence 6, Appl
31	460	72.7	120	12	US-10-025-687-4	Sequence 4, Appl
32	459.5	72.6	449	10	US-09-736-371B-21	Sequence 21, Appl
33	457	72.2	98	10	US-09-840-459-41	Sequence 41, Appl
34	455	71.9	120	10	US-09-810-502-34	Sequence 34, Appl
35	455	71.9	133	12	US-10-006-773-9	Sequence 9, Appl
36	454	71.7	98	10	US-09-840-459-44	Sequence 44, Appl
37	454	71.7	120	10	US-09-229-200A-25	Sequence 25, Appl
38	453.5	71.6	117	10	US-09-840-459-83	Sequence 83, Appl
39	453	71.6	120	10	US-09-229-200A-28	Sequence 28, Appl
40	451.5	71.3	119	10	US-09-811-123-3	Sequence 3, Appl
41	451.5	71.3	138	10	US-09-796-744-15	Sequence 15, Appl
42	448.5	70.9	125	10	US-09-840-459-76	Sequence 76, Appl
43	448	70.8	128	10	US-09-840-459-77	Sequence 77, Appl
44	448	70.8	128	10	US-09-840-459-79	Sequence 79, Appl
45	448	70.8	263	9	US-09-956-086-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-144-886-63
; Sequence 63, Application US/09144886
; Patent No. US2002015114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C25 region VH epitope 2
US-09-144-886-63

Query Match 100.0%; Score 633; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.1e-42;
Matches 118: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGGGLVFRGGSGLKSCAASGFTSDYMYWVWROTPEKRLRWATISDGSGYTY 60
DB 1 QVQLQESGGGLVFRGGSGLKSCAASGFTSDYMYWVWROTPEKRLRWATISDGSGYTY 60
QY 61 PSVKGRTFTSRDNNKNNIYLQWSSLSKSEDTAMYSRRIRYDDAMDYWGCGTTVYSS 118
DB 61 PSVKGRTFTSRDNNKNNIYLQWSSLSKSEDTAMYSRRIRYDDAMDYWGCGTTVYSS 118

RESULT 2
US-09-144-886-62
; Sequence 62, Application US/09144886
; Patent No. US2002015114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D

```

; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentln Ver. 2.0
; LENGTH: 118
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C39 region VH epitope 2
US-09-144-886-62
```

```

Query Match          94.3%; Score 597; DB 9; Length 118;
Best Local Similarity 94.1%; Pred. No. 6.3e-40;
Matches 111; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```

QY 1 QVOLOESGGGLVPRGSLKLSCAASGFTFSDYMWYWRQTPERKLEWVATISDGGSTYY 60
Db 1 QVOLOESGGGLVPRGSLKLSCAASGFTFSDYMWYWRQTPERKLEWVATISDGGSTYY 60
QY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRYRYDDAMDYWGOGTIVTVSS 118
Db 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRYRYDDAMDYWGOGTIVTVSS 118
```

```

RESULT 3
US-09-144-886-65
; Sequence 65, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentln Ver. 2.0
; LENGTH: 118
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 3C3 region VH epitope 2
US-09-144-886-65
```

```

Query Match          82.5%; Score 522; DB 9; Length 118;
Best Local Similarity 83.9%; Pred. No. 3.8e-34;
Matches 99; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
```

```

QY 1 QVOLOESGGGLVPRGSLKLSCAASGFTFSDYMWYWRQTPERKLEWVATISDGGSTYY 60
Db 1 EVKLKESGGGLVPRGSLKLSCAASGFTFSSYAMSWYRQTPERKLEWVATISDGGSTYY 60
QY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRYRYDDAMDYWGOGTIVTVSS 118
Db 61 TDVWKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCARNLPHYHDVWVGOGTIVTVSS 118
```

```

RESULT 4
US-09-144-886-64
; Sequence 64, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
```

```

; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentln Ver. 2.0
; LENGTH: 118
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 2G5 region VH epitope 2
US-09-144-886-64
```

```

Query Match          82.0%; Score 519; DB 9; Length 118;
Best Local Similarity 83.9%; Pred. No. 6.5e-34;
Matches 99; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
```

```

QY 1 QVOLOESGGGLVPRGSLKLSCAASGFTFSDYMWYWRQTPERKLEWVATISDGGSTYY 60
Db 1 EVKLKESGGGLVPRGSLKLSCAASGFTFSSYAMSWYRQTPERKLEWVATISDGGSTYY 60
QY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRYRYDDAMDYWGOGTIVTVSS 118
Db 61 TDVWKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCARNLPHYHDVWVGOGTIVTVSS 118
```

```

RESULT 5
US-09-881-823-12
; Sequence 12, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln version 3.0
; LENGTH: 144
; TYPE: PRF
; ORGANISM: Murline
US-09-881-823-12
```

```

Query Match          81.9%; Score 518.5; DB 10; Length 144;
Best Local Similarity 82.3%; Pred. No. 8.5e-34;
Matches 102; Conservative 5; Mismatches 8; Indels 9; Gaps 2;
```

```

QY 2 QVOLOESGGGLVPRGSLKLSCAASGFTFSDYMWYWRQTPERKLEWVATISDGGSTYY 61
Db 21 VKLVESGGGLVPRGSLKLSCAASGFTFSSYAMSWYRQTPERKLEWVATISDGGSTYY 80
QY 62 DSVKGRFTTISRDNKNNLYLQMSLSKSEDTAMYYCSR-----YRDDAMDYWGOGTIV 114
Db 81 DSVKGRFTTISRDNKNNLYLQMSLSKSEDTAMYYCSRSDGSGSYYY--AMDYWGOGTSV 138
```

```

QY 115 TVSS 118
Db 139 TVSS 142

RESULT 6
US-09-144-886-60
```

; Sequence 60, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 60
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 1A1 region VH epitope 2
US-09-144-886-60

Query Match 80.8%; Score 511.5; DB 9; Length 123;
Best Local Similarity 78.9%; Pred. No. 2.6e-33;
Matches 97; Conservative 9; Mismatches 12; Indels 5; Gaps 1;

OY 1 OVQLOESGGGLVKGPGSLKLSGASGFTFSDYMWVWVROTPKRLWVATISDGGSTYY 60

DB 1 EVKLVESSGGGLVKGPGSLKLSGASGFTFSDYMWVWVROTPKRLWVATISDGGSTYY 60

OY 61 PDSVAGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRYYD-----AMDYWGQGTYY 115

DB 61 PDSVAGRTTISRDNKNNLYLQMSLSKSEDTAMYYCVRHGYCNTPSHWTFDYGAGTYY 120

OY 116 VSS 118
DB 121 VSS 123

RESULT 7
US-09-286-240-4
; Sequence 4, Application US/09286240
; Patent No. US20020010320A1
; GENERAL INFORMATION:
; APPLICANT: Felt; James W
; TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin
; FILE REFERENCE: 110498/74073
; CURRENT APPLICATION NUMBER: US/09/286,240
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-286-240-4

Query Match 80.2%; Score 507.5; DB 10; Length 140;
Best Local Similarity 81.8%; Pred. No. 5.8e-33;
Matches 99; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

OY 1 OVQLOESGGGLVKGPGSLKLSGASGFTFSDYMWVWVROTPKRLWVATISDGGSTYY 60

DB 20 EVMLESGGGLVKGPGSLKLSGASGFTFSSYTWVWVROTPKRLWVATISGSGNTYY 79

OY 61 PDSVAGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSR---YRDDAMDYWGQGTYY 117

DB 80 PDSVAGRTTISRDNKNNLYLQMSLSKSEDTALYYCTRIGDYGAVTMDYWGQGTYY 139

OY 118 S 118
DB 140 S 140

RESULT 8
US-09-144-886-67
; Sequence 67, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 67
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 3H4 region VH epitope 2
US-09-144-886-67

Query Match 79.6%; Score 504; DB 9; Length 118;
Best Local Similarity 81.4%; Pred. No. 9.3e-33;
Matches 96; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

OY 1 OVQLOESGGGLVKGPGSLKLSGASGFTFSDYMWVWVROTPKRLWVATISDGGSTYY 60

DB 1 EVKLVESSGGGLVKGPGSLKLSGASGFTFSSYTWVWVROTPKRLWVATISDGGSTYY 60

OY 61 PDSVAGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRYYDAMDYWGQGTYY 118

DB 61 TDVAGRTTISRDNKNNLYLQMSLSKSEDTAMYYCARLPHYDHYWGQGTYY 118

RESULT 9
US-09-144-886-66
; Sequence 66, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 66
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 3F4 region VH epitope 2
US-09-144-886-66

Query Match 79.5%; Score 503; DB 9; Length 118;
Best Local Similarity 82.8%; Pred. No. 1.1e-32;
Matches 96; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 3 QLOESGGGLVKGPGSLKLSGASGFTFSDYMWVWVROTPKRLWVATISDGGSTYY 62

DB 3 KLVESSGGGLVKGPGSLKLSGASGFTFSSYTWVWVROTPKRLWVATISDGGSTYY 62

OY 63 SVKGRFTTISRDNKNNLYLQMSLSKSEDTAMYYCSRYYDDAMDYWGQGTYY 118

DB 63 NVKGRFTTISRDNKNNLYLQMSLSKSEDTAMYYCARNLPHYDHYWGQGTYY 118

RESULT 10

```
US-09-423-800-46
; Sequence 46, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIAKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 46
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-46

Query Match          79.1%; Score 501; DB 9; Length 118;
Best Local Similarity 81.4%; Pred. No. 1.6e-32;
Matches 96; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVLOESGGGLVPRGSGSLKSCAASGFTSDYMYWVWROTPEKRLKLEWVATISDGGSYTY 60
DB 1 EVVLVEGGGLVPRGSGSLKSCAASGFTFSSYGMWIRQTPDKRLEWVATISDGGSYTY 60

QY 61 PDSVKGFTISRDNANKNTLYLQMSLSKSEDTAMFYCARQTTMTYFAVWGCTVTYSS 118
DB 61 PDSVKGFTISRDNANKNTLYLQMSLSKSEDTAMFYCARQTTMTYFAVWGCTVTYSSA 118

RESULT 11
US-09-423-800-76
; Sequence 76, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIAKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 76
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-76

Query Match          79.1%; Score 501; DB 9; Length 137;
Best Local Similarity 81.4%; Pred. No. 1.8e-32;
Matches 96; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVLOESGGGLVPRGSGSLKSCAASGFTSDYMYWVWROTPEKRLKLEWVATISDGGSYTY 60
DB 20 EVVLVEGGGLVPRGSGSLKSCAASGFTFSSYGMWIRQTPDKRLEWVATISDGGSYTY 79

QY 61 PDSVKGFTISRDNANKNTLYLQMSLSKSEDTAMFYCARQTTMTYFAVWGCTVTYSS 118
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DB 80 PDSVKGFTISRDNANKNTLYLQMSLSKSEDTAMFYCARQTTMTYFAVWGCTVTYSSA 137

RESULT 12
US-10-006-773-4
; Sequence 4, Application US/10006773
; Patent No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor A
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 4
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-4

Query Match          78.0%; Score 493.5; DB 12; Length 140;
Best Local Similarity 79.3%; Pred. No. 7e-32;
Matches 96; Conservative 7; Mismatches 15; Indels 3; Gaps 1;

QY 1 QVLOESGGGLVPRGSGSLKSCAASGFTSDYMYWVWROTPEKRLKLEWVATISDGGSYTY 60
DB 20 EVVLVEGGGLVPRGSGSLKSCAASGFTFSSYGMWIRQTPDKRLEWVATISDGGSHYTY 79

QY 61 PDSVKGFTISRDNANKNTLYLQMSLSKSEDTAMFYCARQTTMTYFAVWGCTVTYSS 117
DB 80 PDSVKGFTISRDNANKNTLYLQMSLSKSEDTALTYCARQTDGAMFEDVWGAGTIVYS 139

QY 118 S 118
DB 140 S 140

RESULT 13
US-10-027-770-5
; Sequence 5, Application US/10027770
; Patent No. US20020151684A1
; GENERAL INFORMATION:
; APPLICANT: MATER, BRUCE
; APPLICANT: SARSELA, KALLE
; APPLICANT: KIRCHAUSEN, TOMAS
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
; FILE REFERENCE: 701039-050001-C
; CURRENT APPLICATION NUMBER: US/10/027,770
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: PCT/US00/17929
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/141,896
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Unknown Organism
FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a
; OTHER INFORMATION: second-generation ScFv derived from monoclonal
; OTHER INFORMATION: antibody 9E10 with site directed mutagenesis
US-10-027-770-5

Query Match          76.5%; Score 484.5; DB 12; Length 269;
Best Local Similarity 75.6%; Pred. No. 6.3e-31;
Matches 96; Conservative 9; Mismatches 13; Indels 9; Gaps 2;
```

us-09-144-886-63.rapb

Page 5

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RESULT 14
US-10-027-770-2
Sequence 2, Application US/10027770
Patent No. US20020151684A1
GENERAL INFORMATION:
APPLICANT: MAYER, BRUCE
APPLICANT: SAKSELA, KALLE
APPLICANT: KIRCHHAUSEN, TOMAS
TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
FILE REFERENCE: /701039-050001-C
CURRENT APPLICATION NUMBER: US/10/027,770
CURRENT FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: PCT/US00/17929
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 60/141,896
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 269
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: 3DX, a
OTHER INFORMATION: second-generation ScFv derived from monoclonal
US-10-027-770-2

```

RESULT 15
US-09-229-200A-6
Sequence 6, Application US/09229200A
Patent No. US20020099179A1
GENERAL INFORMATION:
APPLICANT: Jolliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
CITY: New Brunswick
STATE: NJ
COUNTRY: USA
ZIP: 08933-7003

[illegible]

Search completed: January 13, 2003, 15:14:04
Job time : 9.2087 secs

GENERAL INFORMATION:

APPLICANT: CARCELLER, Ana

APPLICANT: ROSELL, Elisabet

APPLICANT: GOMEZ, Alicia

APPLICANT: ADEN, Jaume

APPLICANT: PILATS, Jaume
TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
TITLE OF INVENTION: Immune response against epidermal growth factor receptor.
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,402B
FILING DATE: 24-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95107967.2
FILING DATE: 26-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: MERCK 1781
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-653-402B-2

Query Match 84.0%; Score 532; DB 2; Length 159;
Best Local Similarity 80.5%; Pred. No. 4.3e-46;
Matches 103; Conservative 6; Mismatches 7; Indels 12; Gaps 2;

QY 1 QVLOESGGGLVPRGSGSLKSCASGFTFSDYVWVWRQTEPKRLEWVATISDGSYTY 60
:|||||
DB 20 EVQLVESGGGLVPRGSGSLKSCASGFTFSDYVWVWRQTEPKRLEWVATISDGSYTY 79
:|||||
QY 61 PDVSKGFTTSDRNKAKNNLYLQNSLSKSEPTAMYYCSR-----YKRDAMDYWGQ 110
:|||||
DB 80 PDVSKGFTTSDRNKAKNNLYLQNSLSKSEPTAMYYCFARDGAARTSSQVYYY--GMDYWGQ 137
:|||||
QY 111 GTTVYSS 118
:|||||
DB 138 GTTVYSS 145

RESULT 3
PCT-US94-14106-59
Sequence 59, Application PC/TUS9414106
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Process for Generating Specific Antibodies
NUMBER OF SEQUENCES: 61
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14106
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:

LENGTH: 217 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14106-59

Query Match 82.5%; Score 522.5; DB 5; Length 217;
Best Local Similarity 84.7%; Pred. No. 5.4e-45;
Matches 100; Conservative 6; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVLOESGGGLVPRGSGSLKSCASGFTFSDYVWVWRQTEPKRLEWVATISDGSYTY 60
:|||||
DB 1 EVQLVESGGGLVPRGSGSLKSCASGFTFSDYVWVWRQTEPKRLEWVATISDGSYTY 60
:|||||
QY 61 PDVSKGFTTSDRNKAKNNLYLQNSLSKSEPTAMYYCSRYRDAMDYWGQGTIVYSS 118
:|||||
DB 61 ADVSKGFTTSDRNKAKNNLYLQNSLSKSEPTAMYYCAR---DPLVSGMGGTITVSS 115
:|||||

RESULT 4
US-08-553-497A-18
Sequence 18, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTERBOURGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSON, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PILATS, JAUME
TITLE OF INVENTION: ANTI-BEGR SINGLE-CHAIN FVS AND ANTI-BEGR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD, SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-553-497A-18

Query Match 80.6%; Score 510.5; DB 2; Length 239;
Best Local Similarity 84.0%; Pred. No. 9,6e-44;
Matches 100; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 1 OVQLOESGGGLVKGSGSLKLSGASGFTFSDYYWVWVROTPEKRLKLEWVATISDGGSTYY 60
DB 1 EVKLDESGLDLVKGSGSLKLSGASGFTFSSYGMWVROTPEKRLKLEWVATISGGAIVY 60
QY 61 PDSVKGRTISRDNKNNLYLQMSLSKSEDTAMYYCSRYRDD-AMDYWGCGTIVYSS 118
DB 61 PDSVKGRTISRDNKNNLYLQMSLSKSEDTAMYYCARLETGDYALDYWGCGTIVYSS 119

RESULT 5
PCT-US93-08435-10

Sequence 10, Application PC/TUS9308435

GENERAL INFORMATION:

APPLICANT: SmithKline Beecham, Corporation

APPLICANT: U.S. Government, Secretary of

APPLICANT: the Navy

APPLICANT: U.S. Government, Secretary of

APPLICANT: the Army

TITLE OF INVENTION: Novel Antibodies for Confering Passive

TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESS: Howson and Howson

STREET: Box 457, 321 Norristown Road

CITY: Spring House

STATE: PA

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08435

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/941,654

FILING DATE: 09-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: SBC P50107

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 540-9200

TELEFAX: (215) 540-5818

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US93-08435-10

Query Match 79.6%; Score 504; DB 5; Length 118;

Best Local Similarity 82.9%; Pred. No. 1,9e-43;

Matches 97; Conservative 7; Mismatches 9; Indels 4; Gaps 2;

QY 6 ESGGGLVKGSGSLKLSGASGFTFSDYYWVWVROTPEKRLKLEWVATISDGGSTYYDSVK 65
DB 2 ESGGGLVKGSGSLKLSGASGFTFSSYGMWVROTPEKRLKLEWVATISDGGSTYYDVTY 61
QY 66 GRTISRDNKNNLYLQMSLSKSEDTAMYYCSR--YRYDD-AMDYWGCGTIVYSS 118
DB 62 GRTISRDNKNNLYLQMSLSKSEDTAMYYCASLIYGYDGYAMDYWGCGTIVYSS 118

RESULT 6
US-08-331-398A-61

Sequence 61, Application US/08331398A

Patent No. 5608039

GENERAL INFORMATION:

APPLICANT: Paston, Ira

APPLICANT: Willingham, Mark

APPLICANT: Fitzgerald, David

APPLICANT: Brinkmann, Ulrich

APPLICANT: Pal, Lee

TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins

TITLE OF INVENTION: and Their Uses (as amended)

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Crew

STREET: One Market Plaza, Stewart Street Plaza

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/331,398A

FILING DATE: 28-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/767,331

FILING DATE: 30-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/596,289

FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 015280-126110US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 137 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Region

LOCATION: 1..137

OTHER INFORMATION:

OTHER INFORMATION: /note="Mouse monoclonal antibody B1 Fv

US-08-331-398A-61

Query Match 79.5%; Score 503.5; DB 1; Length 137;

Best Local Similarity 82.6%; Pred. No. 2,5e-43;

Matches 100; Conservative 4; Mismatches 14; Indels 3; Gaps 2;

QY 1 OVQLOESGGGLVKGSGSLKLSGASGFTFSDYYWVWVROTPEKRLKLEWVATISDGGSTYY 60
DB 1 EVKLDESGLDLVKGSGSLKLSGASGFTFSDNYWVWVROTPEKRLKLEWVATISDGGSTYID 60
QY 61 PDSVKGRTISRDNKNNLYLQMSLSKSEDTAMYYCSR--YRYDDA-MDYWGCGTIVYSS 117
DB 61 PDSVKGRTISRDNKNNLYLQMSLSKSEDTAMYYCARSPYIDYAPFTYWGCGTIVYSS 120
QY 118 S 118
DB 121 A 121

RESULT 7

US-08-331-397B-61
Sequence 61, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..137
OTHER INFORMATION: /note="Mouse monoclonal antibody B1 Fv
OTHER INFORMATION: Heavy chain region"
US-08-331-397B-61

Query Match 79.5%; Score 503.5; DB 2; Length 137;
Best Local Similarity 82.6%; Pred. No. 2.5e-43;
Matches 100; Conservative 4; Mismatches 14; Indels 3; Gaps 2;

QY 1 QVQLQESGGGLVPGGSLKISCAASGFTPSDYYMWVWRQTPERKRLMVAATISDGGSYTY 60
:|||||
DB 1 EVQLVDSGGGLVPGGSLKISCAASGFTPSDNYMWVWRQTPERKRLMVAATISDGGTYIDY 60
QY 61 PDSVKGRTISRDNANKNNLYLQSSLSKSEDTAMYYCSR--YRDDA-MDYWGCGTIVTVS 117
:|||||
DB 61 SDSVKGRTISRDNANKNNLYLQSSLSRSEDTGMYYGCRSPYYDYAPFTYWGCGTIVTVS 120
QY 118 S 118
DB 121 A 121

RESULT 8

US-08-759-804A-60
Sequence 60, Application US/08759804A
Patent No. 5990296
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David J.
APPLICANT: Brinkmann, Ulrich
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..137
OTHER INFORMATION: /note="Mouse monoclonal antibody B1 Fv
OTHER INFORMATION: Heavy chain region"
US-08-759-804A-60

Query Match 79.5%; Score 503.5; DB 2; Length 137;
Best Local Similarity 82.6%; Pred. No. 2.5e-43;
Matches 100; Conservative 4; Mismatches 14; Indels 3; Gaps 2;

QY 1 QVQLQESGGGLVPGGSLKISCAASGFTPSDYYMWVWRQTPERKRLMVAATISDGGSYTY 60
:|||||
DB 1 EVQLVDSGGGLVPGGSLKISCAASGFTPSDNYMWVWRQTPERKRLMVAATISDGGTYIDY 60
QY 61 PDSVKGRTISRDNANKNNLYLQSSLSKSEDTAMYYCSR--YRDDA-MDYWGCGTIVTVS 117
:|||||
DB 61 SDSVKGRTISRDNANKNNLYLQSSLSRSEDTGMYYGCRSPYYDYAPFTYWGCGTIVTVS 120
QY 118 S 118
DB 121 A 121

Db 121 A 121

RESULT 9
US-08-356-272-3
; Sequence 3, Application US/08356272
; Patent No. 5766946
; GENERAL INFORMATION:
; APPLICANT: Clantiglia Dr., Maurizio
; TITLE OF INVENTION: Monoclonal Antibodies to glycoprotein P
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent and Trademark Department, Sandoz
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: N. J.
; COUNTRY: U. S. A.
; ZIP: 07936
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356, 272
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
CLASSIFICATION: C12N5/20
CLASSIFICATION: G01N33/574
CLASSIFICATION: G01N33/577
CLASSIFICATION: A61K39/295
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM92A000457
FILING DATE: 17-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP93/01533
FILING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Battle, Carl W.
REGISTRATION NUMBER: 30,731
REFERENCE/DOCKET NUMBER: 118-8040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 503-8177
TELEFAX: (201) 503-8807
TELEX: 240867
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-272-3

Query Match 79.3%; Score 502; DB 1; Length 123;
Best Local Similarity 82.8%; Pred. No. 3.2e+43;
Matches 101; Conservative 5; Mismatches 12; Indels 4; Gaps 2;

Qy 1 QVQLQESGGGLVYK-PGSGSLKSCAASGFTSDYMYWVWVROTPEKRLRWATISDGSSTYY 59
Db 1 QVQLQESGGDLVKDPGSLKSCAASGFTFSRYGMSWVWQTDKRLRWATISDGSSTYY 60
Qy 60 YPDSYKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSR--YRIDDADMYGCGTTVTY 116
Db 61 PDSYKGRFTISRDNKNNLYLQVWSLSKSEDTAMYYCARPAEFKRGYSWFAWVGCGTTVTY 120
Qy 117 SS 118
Db 121 SS 122

RESULT 10
US-08-331-398A-65

; Sequence 65, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION: /note="Mouse monoclonal antibody B5 Fv
US-08-331-398A-65

Query Match 78.9%; Score 499.5; DB 1; Length 125;
Best Local Similarity 80.7%; Pred. No. 5.7e+43;
Matches 96; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

Qy 1 QVQLQESGGGLVYKPGSGSLKSCAASGFTSDYMYWVWVROTPEKRLRWATISDGSSTYY 60
Db 1 EVKLVESGGGLVQPGSGSLKSCATSGFTSDYMYWVWVROTPEKRLRWATISDGSSTYY 60
Qy 61 PDSYKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSRYYDDA-MDYVGCGTTVTYSS 118
Db 61 PDSYKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCARGLSDGSWFAWVGCGTTVTYSS 119
Qy 117 SS 118
Db 121 SS 122

RESULT 11
US-08-331-397B-65
; Sequence 65, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira

APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-12612005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ. ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION: /note="Mouse monoclonal antibody B5 Fv
OTHER INFORMATION: Heavy chain region"
US-08-331-397B-65
Query Match 78.9%; Score 499.5; DB 2; Length 125;
Best Local Similarity 80.7%; Pred. No. 5.7e-43;
Matches 96; Conservative 7; Mismatches 15; Indels 1; Gaps 1;
QY 1 QVLOESGGGLVPRGSGIKSCASGFTSDYMWYWRQTPERKLEWVAITSDGGSITY 60
DB 1 EVLVESGGGLVPGGSLKSCATSGFTSDYMWYWRQTPERKLEWVAITSDGGSITY 60
QY 61 PDSVKGRTTSRDNANKNLTLQMSLSKSEPTAMYYCSRYRYDDA-MDYWGQGTTVYSS 118
DB 61 PDIVKGRFTIDRNANKNTLYLQMSRLKSEPTAMYYCARGLSDGSWPAWYGQGLTVYSS 119
RESULT 12
US-08-759-804A-64
Sequence 64, Application US/08759804A
Patent No. 5990296
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Wittingham, Mark
APPLICANT: Fitzgeraid, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pal, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof

NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-12614005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION: /note="Mouse monoclonal antibody B5 Fv
OTHER INFORMATION: Heavy chain region"
US-08-759-804A-64
Query Match 78.9%; Score 499.5; DB 2; Length 125;
Best Local Similarity 80.7%; Pred. No. 5.7e-43;
Matches 96; Conservative 7; Mismatches 15; Indels 1; Gaps 1;
QY 1 QVLOESGGGLVPRGSGIKSCASGFTSDYMWYWRQTPERKLEWVAITSDGGSITY 60
DB 1 EVLVESGGGLVPGGSLKSCATSGFTSDYMWYWRQTPERKLEWVAITSDGGSITY 60
QY 61 PDSVKGRTTSRDNANKNLTLQMSLSKSEPTAMYYCSRYRYDDA-MDYWGQGTTVYSS 118
DB 61 PDIVKGRFTIDRNANKNTLYLQMSRLKSEPTAMYYCARGLSDGSWPAWYGQGLTVYSS 119
RESULT 13
US-08-579-378A-16
Sequence 16, Application US/08579378A
Patent No. 6210671
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/579, 378A
APPLICATION NUMBER: US/08/579, 378A
FILING DATE: 27-DEC-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschultz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-002220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-579-378A-16

Query Match 78.8%; Score 499; DB 4; Length 135;
Best Local Similarity 83.1%; Pred. No. 7e-43;
Matches 98; Conservative 8; Mismatches 10; Indels 2; Gaps 2;

Qy 1 OVOLDESGGLVPGGSLKSCAAGFTSDYYWVWVROTPEKRLBMTATISDGGSTYY 60
Db 20 EVKLVEGGGLVPGGSLKLACASGFTSTYAMSWVROTPEKRLBMTATISDGGSTYY 78
Qy 61 PDSVGRFTISRDNAKNNLYLQMSSLSKSEDTAMYYCSRYRDAMDYWGCGTTVYSS 118
Db 79 PDSVGRFTISRDNAKNNLYLQMSSLSKSEDTAMYYCAR-DYDGYFDYWGCGTTVYSS 135

RESULT 14
US-08-661-052-4
Sequence 4, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deco
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezlan Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-661-052-4

Query Match 78.5%; Score 497; DB 2; Length 300;
Best Local Similarity 76.7%; Pred. No. 2.8e-42;
Matches 92; Conservative 13; Mismatches 13; Indels 2; Gaps 1;

Qy 1 OVOLDESGGLVPGGSLKSCAAGFTSDYYWVWVROTPEKRLBMTATISDGGSTYY 60
Db 1 EVOLVESGGGVQPGSLKSLSCSSSGFTSDNYMYVRAPKGLBMTATISDGGSTYY 60
Qy 61 PDSVGRFTISRDNAKNNLYLQMSSLSKSEDTAMYYCSR--YRYDDAMDYWGCGTTVYSS 118
Db 61 PDSVGRFTISRDNSKNTFLQMDSLRPDGTGYFCARGYRYREGAMDYWGCGTPTVYSS 120

RESULT 15
US-09-188-082-4
Sequence 4, Application US/09188082
Patent No. 6270765
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deco
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezlan Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 300 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 US-09-188-082-4

Query Match 78.5%; Score 497; DB 4; Length 300;
 Best Local Similarity 76.7%; Pred. No. 2.8e-42;
 Matches 92; Conservative 13; Mismatches 13; Indels 2; Gaps 1;

QY 1 OVOIQESGGIVKPGSLKISCAASGFTFSDYVWYVROTPEKRLKLEWVATISDGSSTYY 60
 Db 1 EVOLVESGGGVOPGRSLRLSCSSSGFIFSDNMYWVWQAPGKGLEWVATISDGSSTYY 60
 QY 61 PDSYKGRFTISRDNKNNLYLQMSLSKSEPTAMYYCSR--YRYDDADYWGOGTTVYSS 118
 Db 61 PDSYKGRFTISRDNKNNLYLQMSLSKSEPTAMYYCSR--YRYDDADYWGOGTTVYSS 120

Search completed: January 13, 2003, 15:13:42
 Job time: 12.8 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:07:08 ; Search time 31.8087 Seconds
(without alignments)
494.317 Million cell updates/sec

Title: US-09-144-886-63

Perfect score: 633
Sequence: 1 QVQLQESGGGLVFRGGSGLK.....YRVDAMDYMGCGITTVYSS 118

Scoring table

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A-Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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- 10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
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- 16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
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- 18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575.5	90.9	123	AA151266	Monoclonal antbod
2	568	89.7	120	AA151266	FC receptor Mab 02
3	550	86.9	115	AA151266	IGG monoclonal ant
4	532.5	84.1	142	AA151266	Antibody 4A2 heavy
5	532.5	84.1	249	AA151266	Anti-Fix/FixA anti
6	532.5	84.0	159	AA151266	Mouse anti-Idiotyp
7	522.3	82.5	217	AA151266	Mouse antibody H3-
8	520.5	82.2	119	AA151266	Humanised mouse TR
9	520.5	82.2	464	AA151266	TRA-8 heavy chain.
10	519	82.0	120	AA151266	EGF receptor chime

11	513.5	81.1	119	AA151266	Anti-EGFR antibody
12	513.5	81.1	119	AA151266	Heavy chain variab
13	513	81.0	118	AA151266	Human Ige receptor
14	510.5	80.6	119	AA151266	Anti-EGFR antibody
15	510.5	80.6	138	AA151266	Mouse anti-verotox
16	510.5	80.6	239	AA151266	Anti-EGFR single c
17	509.5	80.5	117	AA151266	Human Ige receptor
18	509.5	80.5	117	AA151266	Heavy chain variab
19	509.5	80.5	117	AA151266	Heavy chain variab
20	507.5	80.2	119	AA151266	Anti-EGFR antibody
21	507.5	80.2	121	AA151266	Human anti-DAF ant
22	507.5	80.2	140	AA151266	Mouse monoclonal a
23	506.5	80.0	143	AA151266	Heavy chain (VH) g
24	505.5	79.9	121	AA151266	Mouse antibody 2A4
25	504.5	79.7	120	AA151266	Op-G2 monoclonal a
26	504	79.6	118	AA151266	Mab NF52 heavy cha
27	504	79.6	118	AA151266	Human Ige receptor
28	503.5	79.5	119	AA151266	Humanised mouse TR
29	502.5	79.4	138	AA151266	MRK16-H chain. Ch
30	502.5	79.4	139	AA151266	hCEA specific mus
31	502.5	79.4	140	AA151266	Mouse mab 26-2F he
32	502	79.3	123	AA151266	Heavy chain variab
33	501	79.1	118	AA151266	Chimeric H chain S
34	501	79.1	118	AA151266	Mouse humanised an
35	501	79.1	118	AA151266	Peptide seq ID No:
36	501	79.1	118	AA151266	Amino acid sequenc
37	501	79.1	118	AA151266	Mouse anti-PTHrP m
38	501	79.1	118	AA151266	Human PTHrP mouse
39	501	79.1	118	AA151266	Human PTHrP mouse
40	501	79.1	118	AA151266	Human PTHrP mouse
41	501	79.1	118	AA151266	Mouse joint diseas
42	501	79.1	137	AA151266	Chimeric antibody
43	501	79.1	137	AA151266	Mouse humanised an
44	501	79.1	137	AA151266	Mouse antibody H c
45	501	79.1	137	AA151266	Amino acid sequenc

ALIGNMENTS

RESULT 1	AA151266	standard: peptide; 123 AA.
ID	AA151266	
AC	AA151266	
DT	14-APR-2000	(first entry)
DE	Monoclonal antibody MAK 33 heavy chain variable region peptide.	
KW	Framework region; monoclonal antibody; variable domain; detection; immunotherapy; MAK 33.	
OS	Unidentified.	
XX	DE19828466-A1.	
XX	30-DEC-1999.	
XX	26-JUN-1998;	98DE-1028466.
XX	26-JUN-1998;	98DE-1028466.
XX	26-JUN-1998;	98DE-1028466.
XX	(HOFF) ROCHE DIAGNOSTICS GMBH.	
XX	Nussbaum S, Moesner E, Lenz H, Praest G;	
XX	WPI; 2000-107255/10.	
XX	Suppressor peptides derived from antibodies for use in immunoassays	
XX	Disclosure; Page 18; 20pp; German.	

CC This invention describes novel peptides derived from a framework region
CC of the variable domain of an antibody for detection, immunotherapy or
CC for scintigraphy. The peptides of the invention are used in a method to
CC detect analytes in a sample by eliminating interference in the sample.
CC AA51254.Y51267 represent peptides derived from the framework regions of
CC the variable domain of an antibody which are used to illustrate the
CC method of the invention.

CC Sequence 123 AA:

Query Match 90.9%; Score 575.5; DB 21; Length 123;
Best Local Similarity 89.4%; Pred. No. 3e-46;

Matches 110; Conservative 4; Mismatches 4; Indels 5; Gaps 1;

QY 1 QVLOESGGGLVPRGSLKSCAASGFTSDYMWVWROTPERKLEWVATISDGGSTYY 60
Db 1 EVQVSEGGGLVPRGSLKSCAASGFTSDYMWVWROTPERKLEWVATISDGGSTYY 60
QY 61 PDSYKGRFTISRDNKAKNNLYLQMSLSKSEPTAMVYCSRRY---YDAMDYWGQGTYY 115
Db 61 PDSYKGRFTISRDNKAKNNLYLQMSLSKSEPTAMVYCARDAKAYGNYGDMYWGQGTYY 120
QY 116 VSS 118
Db 121 VSS 123

RESULT 2

AAR54931
ID AAR54931 standard; peptide; 120 AA.

AC AAR54931;

DT 19-OCT-1994 (first entry)

DE Fc receptor Mab 022 VH chain.

XX Fc receptor; FcR; humanized antibody; hab; IgG; cancer; allergy;

XX autoimmune disease; heteroantibody; bifunctional antibody;

XX immunotoxin; CDR; complementarity determining region; VH;

XX heavy chain variable region; VK; kappa chain variable region;

XX mononuclear phagocyte; PCR; polymerase chain reaction; primer;

XX site-directed mutagenesis; monoclonal antibody; Mab.

OS Mus sp.

PN WO9410332-A.

XX 11-MAY-1994.

PD 04-NOV-1993; 93WO-US10384.

PF 04-NOV-1992; 92GB-0023377.

XX (MEDA-) MEDAREX INC.

PA Carr FJ, Harris WJ, Tempest PR;

PI WPI; 1994-167486/20.

XX New humanised antibodies to Fc receptors - used for diagnosis or

XX for treatment of e.g. cancer, allergies and infectious and

XX auto-immune diseases

PS Disclosure; Page 15; 36pp; English.

XX Humanized antibodies (habs) for IgG Fc receptors on human phagocytes

CC comprise the CDR of mouse monoclonal antibody 22 (from hybridoma

CC 022MCL-1), VH chains from human Igs NEMM or KOL, and VK chains from

CC Ig R1. Sequences are provided for mouse 022 VH (AAR54931),

CC humanized NEMM-based VH (022 NMVH, AAR54929), humanized KOL-

CC based VH (022 KLVI, AAR54930), mouse 022 VK (AAR54933) and humanized

CC R1- based VK (022 HUVK, AAR54932). During hab production, VH and VK

CC cDNAs were PCR amplified using primers given in AA065378-87.
CC Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was performed using
CC oligos AA065388-89. The habs can be used in heteroantibody,
CC bifunctional antibody and immunotoxin production.

CC Sequence 120 AA:

Query Match 89.7%; Score 568; DB 15; Length 120;
Best Local Similarity 89.2%; Pred. No. 1.5e-45;

Matches 107; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

QY 1 QVLOESGGGLVPRGSLKSCAASGFTSDYMWVWROTPERKLEWVATISDGGSTYY 60
Db 1 EVQVSEGGGLVPRGSLKSCAASGFTSDYMWVWROTPERKLEWVATISDGGSTYY 60
QY 61 PDSYKGRFTISRDNKAKNNLYLQMSLSKSEPTAMVYCSRRY---YDAMDYWGQGTYY 118
Db 61 PDSYKGRFTISRDNKAKNNLYLQMSLSKSEPTAMVYCARDAKAYGNYGDMYWGQGTYY 120

RESULT 3

AAB12460
ID AAB12460 standard; Protein; 115 AA.

AC AAB12460;

DT 25-OCT-2000 (first entry)

DE IgG monoclonal antibody protein sequence SEQ ID NO:6.

XX Monoclonal antibody; hybridoma cell; immunoglobulin; IgG; fusion;

XX human albumin; diabetic nephropathy; diagnosis.

XX Mus musculus.

PN JP2000139460-A.

PD 23-MAY-2000.

PF 02-NOV-1998; 98JP-0311677.

PR 02-NOV-1998; 98JP-0311677.

PA (TOYOTA) TOYOTA CHUO KENKYUSHO KK.

XX (AISE) AISEI SEIKI KK.

DR WPI; 2000-433935/38.

XX N-PSDB; AAA60723.

XX Hybridoma cells for preparation of IgG monoclonal antibody capable of

XX rapid reaction with human albumin for diagnosis of diabetic nephropathy

XX Disclosure; Page 8; 11pp; Japanese.

XX The present invention describes hybridoma cells used for preparing an

XX immunoglobulin G (IgG) monoclonal antibody capable of rapid reaction

XX with human albumin. The hybridoma cells are prepared by fusion of mamal

XX myeloma cells and spleen cells immunised with human serum albumin, and

XX producing IgG monoclonal antibody which rapidly react with human

XX albumin. The monoclonal antibodies can be used in the diagnosis of

XX diabetic nephropathy. The present sequence represents an IgG monoclonal

XX antibody protein sequence from the present invention.

PS Sequence 115 AA:

Query Match 86.9%; Score 550; DB 21; Length 115;
Best Local Similarity 89.7%; Pred. No. 6.7e-44;

Matches 105; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 2 VQLOESGGGLVPRGSLKSCAASGFTSDYMWVWROTPERKLEWVATISDGGSTYY 61

Db 1 VQLOESGGGLVPRGSLKSCAASGFTSDYMWVWROTPERKLEWVATISDGGSTYY 60

QY 62 DSVKGRFTISRDNANKNNLYLQMSLSKSEDTAMYYCSRYRDAMDYWGCGTTVTYSS 118
 DB 61 DSVKGRFTISRDNANKNNLYLQMSLSKSEDTAMYYCYVREGMNGA--YWGCGTTVTYSS 115

RESULT 4

AAR30882 ID AAR30882 standard; Protein; 142 AA.

AC AAR30882;

DT 10-MAY-1993 (first entry)

DE Antibody 4A2 heavy chain constant region.

XX Fd'; fragment; human; 4A2; constant region; Fab'; F(ab')2; antibody;
 XX heavy chain; primer.

OS Mus musculus.

PN WO9222324-A.

PD 23-DEC-1992.

PF 15-JUN-1992; 92WO-US04976.

PR 14-JUN-1991; 91US-0714175.

PA (XOMA) XOMA CORP.

PI Better MD, Carroll S, Horwitz AH;

DR WPI: 1993-017909/02.

DR P-PSDB: AAQ34576.

PT Polynucleotide sequences encoding Fab' and F(ab')2 fragments -
 used to produce, e.g. antibody-ricin A chain immuno:toxin(s)

PS Disclosure: Fig 11; 92pp; English.

XX This sequence represents the heavy chain constant domain (CH) from
 CC mouse antibody 4A2. This sequence was used in conjunction
 CC with the Fd' sequences given in AAQ34567-72 to produce chimeric Fd'
 CC vectors.

XX Sequence 142 AA;

Query Match 84.1%; Score 532.5; DB 14; Length 142;
 Best Local Similarity 83.7%; Pred. No. 3,6e-42;
 Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

QY 1 OVQLOESGGGLVPGGSLKLSCAASGFTFSDYMYVVRQTPKRLKLEWVATISDGSITYY 60
 DB 20 EVQLVESGGGLVPGGSLKLSCAASGFTFSDYMYVVRQTPKRLKLEWVATISDGSITYY 79

QY 61 PDSVGRFTISRDNANKNNLYLQMSLSKSEDTAMYYCSR--YKXDA--MDYWGCGTTVT 115
 DB 80 SDSYNGRFTISRDNANKNNLYLQISSLSKSEDTAMYYCARDPYSYDSSPAWFAWVGCGTLVT 139

QY 116 VSS 118

DB 140 VSA 142

DB 140 VSA 142

RESULT 5
 AAB20434 ID AAB20434 standard; Protein; 249 AA.

AC AAB20434;

DT 21-JUN-2001 (first entry)

DE Anti-FIX/FIXa antibody 193/K2 scFv.

XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;

KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;

KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

OS Chimeric - Mus musculus.

XX Chimeric - Synthetic.

XX Key

XX Location/Qualifiers

XX 1..121

XX /label= VH

XX 98..110

XX /label= CDR3

XX 122..135

XX /label= Linker

XX 136..249

XX /label= VL

XX 230..238

XX /label= CDR3

XX WO200119992-A2.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-EP08936.

XX 14-SEP-1999; 99AT-0001576.

XX (BAXT) BAXTER AG.

XX Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;

XX WPI: 2001-290358/30.

XX N-PSDB: AAF30724.

XX New factor IX/factor IXa antibodies and their derivatives useful for

PT increasing amidolytic activity of factor IXa, and for treating blood

PT coagulation disorders such as haemophilia A and haemorrhagic diathesis

PS Claim 10; Fig 15; 138pp; English.

XX The present sequence is that of a single chain Fv (scFv) derivative
 CC of antibody 193/K2, comprising the heavy (VH) and light (VL) chain
 CC variable regions of 193/K2 joined by an artificial, flexible linker
 CC peptide. The scFv was obtained by PCR amplification of cDNAs for
 CC 193/K2 VH and VL regions and cloning in vector pDAp2. 193/K2 is
 CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
 CC antibodies of the invention. Anti-FIX/FIXa and their derivatives,
 CC including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor
 CC activity or FIXa activating activity. Administration leads to an
 CC increase in the procoagulant activity of FIXa, even in the presence
 CC of FVIIIa inhibitors. This allows for rapid blood coagulation even
 CC in the absence of FVIII or FVIIIa, and in the case of FVIII
 CC inhibitor patients. The antibodies and derivatives are used in a
 CC claimed pharmaceutical composition for treating patients with blood
 CC coagulation disorders, especially haemophilia A and haemorrhagic
 CC diathesis.

SQ Sequence 249 AA;

Query Match 84.1%; Score 532.5; DB 22; Length 249;
 Best Local Similarity 84.3%; Pred. No. 6,5e-42;
 Matches 102; Conservative 6; Mismatches 10; Indels 3; Gaps 1;

QY 1 OVQLOESGGGLVPGGSLKLSCAASGFTFSDYMYVVRQTPKRLKLEWVATISDGSITYY 60
 DB 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSDYMYVVRQTPKRLKLEWVATISDGSITYY 60

QY 61 PDSVGRFTISRDNANKNNLYLQMSLSKSEDTAMYYCSR--YKXDA--MDYWGCGTTVT 117
 DB 61 PDSVGRFTISRDNANKNNLYLQMSLSKSEDTAMYYCTRDGCHGYSSFDYWGCGTTVT 120

OY 118 S 118
 Db 121 S 121

RESULT 6
 ID AAM19575 standard; Protein; 159 AA.
 AC AAM19575
 XX
 DT 30-JUL-1997 (first entry)

DE Mouse anti-idiotypic antibody 15H8 heavy chain variable region.
 XX
 KW Anti-idiotypic: anti-EGFR; epidermal growth factor receptor; tumour;
 KM cancer; neoplasia; glioma; melanoma; carcinoma; drug; manufacture; ss.
 XX
 OS Mus musculus.

XX
 FH Key Location/Qualifiers
 FT peptide 1..19
 FT /label= sig-peptide
 FT Region 20..49
 FT /label= FR1
 FT /note= "framework region 1"
 FT Region 50..54
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 55..68
 FT /label= FR2
 FT /note= "framework region 2"
 FT Region 69..85
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 86..117
 FT /label= FR3
 FT /note= "framework region 3"
 FT Region 118..134
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT Region 135..145
 FT /label= FR4
 FT /note= "framework region 4"
 FT Region 146..159
 FT /note= "mouse constant IgG1 region"

XX
 PN EP745612 A1.
 XX
 PD 04-DEC-1996.
 XX
 PF 14-MAY-1996; 96EP-0107651.
 XX
 PR 26-MAY-1995; 95EP-0107967.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Adan J, Carceller A, Gomez A, Pluats J, Rosell E;
 DR WPI; 1997-013659/02.
 DR N-PSDB; AAT70806.
 XX

PT Monoclonal anti-idiotypic antibodies mimicking epidermal growth
 PT factor receptor - useful for tumour therapy
 XX
 PS Claim 6; Fig 5A; 28pp; English.
 XX
 CC Murine monoclonal anti-idiotypic antibodies, 15H8, 3B6 and 5A6 are
 CC new. They induce an immune response against epidermal growth factor
 CC receptor (EGFR). The sequences of the heavy and light chain variable
 CC regions of these antibodies are given in the specification. The
 CC antibodies are used for the manufacture of drugs directed against
 CC tumours that express EGFR on their surface, including melanomas,

CC gliomas and carcinomas.
 XX
 SQ Sequence 159 AA;
 OY
 Query Match 84.0%; Score 532; DB 18; Length 159;
 Best Local Similarity 80.5%; Pred. No. 4.5e-42;
 Matches 103; Conservative 6; Mismatches 7; Indels 12; Gaps 2;

OY 1 OVOLOESGGGLVPGGSLKSCAASGFTFSDYMYWVWVROTPEKRLMVAITSDGSGYTY 60
 Db 20 EVOLVESGGGLVPGGSLKSCAASGFTFSDYMYWVWVROTPEKRLMVAITSDGSGYTY 79
 OY 61 PDSYKGRFTISRDNAKNNLYLQMSLSKSEDTAMYYCSR-----YRYDAMDYWGQ 110
 Db 80 PDSLKGRFTISRDNAKNNLYLQMSLSKSEDTAMYYFCARDGARTSSQVYY--GMDYWGQ 137
 OY 111 GTTYTVYSS 118
 Db 138 GTSYTVYSS 145

RESULT 7
 ID AAR75460 standard; Protein; 217 AA.
 AC AAR75460;
 XX
 DT 07-FEB-1996 (first entry)

DE Mouse antibody H3-3 heavy chain variable region protein sequence.
 XX
 KW Primer: amplification; PCR; mouse; kappa chain; heavy chain; Fab;
 KW antibody; immunotolerance; animal; variegated display library;
 KW variable region; antigen; immunorecessive; cell surface marker; foetal;
 KW cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
 XX
 OS Mus musculus.
 XX
 PN W09515982 A2.
 XX
 PD 15-JUN-1995.
 XX
 PF 08-DEC-1994; 94MO-US14106.
 XX
 PR 06-DEC-1994; 94US-0350400.
 PR 08-DEC-1993; 93US-0164022.
 XX
 PA (GEN2) GENZYME CORP.
 XX
 PI Barsomian G, Copeland DP, Hillhouse D, Johnson T;
 DR WPI; 1995-224291/29.
 DR N-PSDB; AAO92504.
 XX

PT Generating new antibodies specific for immunorecessive epitopes -
 PT by selection from variegated V gene library cloned from
 PT immuno:tolerance derived antibody repertoire; useful in diagnosis,
 PT purifica. and therapy, e.g. of cancer
 XX
 PS Disclosure; Page 82-83; 109pp; English.
 XX

CC The sequence of the heavy chain variable region from the mouse antibody
 CC H3-3. This sequence was isolated from a variegated display library (VDL)
 CC of variable regions derived from a repertoire of antibodies from an
 CC immunotolerised animal. The VDL is generated by PCR amplifying the
 CC variable regions from the antibody coding sequences using the primers
 CC AA074153-74. The variable regions, esp the complementarity determining
 CC regions (CDR; see AAR75462-93 for examples of CDRs) from the
 CC immunotolerant animals' antibodies are used to construct an antibody
 CC against an immunorecessive antigen e.g. a cell surface marker on a foetal,
 CC cancer or stem cell, which can differentiate between variant or related
 CC forms of the antigen. The antibodies generated can be used in the

CC diagnosis, e.g. detection of the immunorecessive antigen, or in therapy
CC e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia.
CC The method of production of the antibody allows rapid and sensitive
CC isolation of antibodies that would be difficult to isolate by standard
CC methods. The antibodies produced have greater binding affinity than
CC those produced by combinatorial/hybridoma methods.
XX
SO Sequence 217 AA;
Query Match 82.5%; Score 522.5; DB 16; Length 217;
Best Local Similarly 84.7%; Pred. No. 4.8e-41;
Matches 100; Conservative 6; Mismatches 9; Indels 3; Gaps 1;
OY 1 QVLOESGGGLVKKPGSGSLKSCAASGFTFSDYMWVWQTPKRLKLEWATISDGGSTYY 60
DB 1 EVKLMESSGGLVKKPGSGSLKSCAASGFTFSDYMWVWQTPKRLKLEWATISDGGSTYY 60
OY 61 PDSYKGRFTISRDNKNNLYLQMSLKSSEDTRAMYYCSRRYRDDAMDYGGGTTVYSS 118
DB 61 ADSYKGRFTISRDNKNNLYLQMSLKSSEDTRAMYYCAR---DPLXSGSGGTTLVYSS 115
RESULT 8
AAU72814
ID AAU72814 standard; Protein: 119 AA.
XX
AC AAU72814;
XX
DT 26-FEB-2002 (first entry)
XX
DE Humanised mouse TRA-8 anti-human DR5 antibody #4.
XX
KW Tumour necrosis factor-related apoptosis-inducing ligand receptor;
KW TRAIL; TRAIL receptor DR5; cytosolic; apoptosis; cell proliferation;
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
XX
OS Synthetic.
XX
PN WO200183560-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14151.
XX
PR 02-MAY-2000; 2000US-201344P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX
DR WPI: 2002-049338/06.
XX
PT Novel antibody specific for tumour necrosis factor-related
PT apoptosis-inducing ligand, useful for inhibiting cell proliferation in
PT cancer -
XX
PS Example 26; Page 212-213; 229pp; English.
XX
CC The invention describes a novel antibody which recognizes a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
CC activity to a cell expressing DR5 in vivo. It is also useful for
CC preparing a therapeutic for selective apoptosis of abnormal or
CC dysregulated cells, and for inhibiting cell proliferation in a cell,
CC preferably a human breast, ovary, colon, haematopoietic, prostate,
CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
CC also be administered e.g. paclitaxel, taxol or cycloheximide. The
CC antibody is used to treat an autoimmune disease, systemic lupus

CC erythematosus, Hashimoto's disease, rheumatoid arthritis.
CC graft-versus-host disease, Sjogren's syndrome, Chron's disease,
CC pernicious anaemia, Addison disease, scleroderma, Goodpasture's syndrome,
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple
CC sclerosis, Basedow's disease, insulin-dependent diabetes mellitus,
CC allergy, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerular nephritis, hypoplastic anaemia, rejection after organ
CC transplantation, and numerous malignancies of lung, prostate, liver,
CC ovary, lymphatic or breast tissue. This sequence shows one of the
CC humanised anti-DR5 antibodies described in the method of the invention.
XX
SO Sequence 119 AA;
Query Match 82.2%; Score 520.5; DB 23; Length 119;
Best Local Similarly 85.0%; Pred. No. 3.9e-41;
Matches 102; Conservative 5; Mismatches 10; Indels 3; Gaps 2;
OY 1 QVLOESGGGLVKKPGSGSLKSCAASGFTFSDYMWVWQTPKRLKLEWATISDGGSTYY 60
DB 1 EYKLMESSGGLVKKPGSGSLKSCAASGFTFSDYMWVWQTPKRLKLEWATISDGGSTYY 60
OY 61 PDSYKGRFTISRDNKNNLYLQMSLKSSEDTRAMYYCSRRYRDDAM--DYWGCGTTVYSS 118
DB 61 PDSYKGRFTISRDNKNNLYLQMSLKSSEDTRAMYYCAR--RQDSMTTDDYWGCGTTLVYSS 119
RESULT 9
AAU72801
ID AAU72801 standard; Protein: 464 AA.
XX
AC AAU72801;
XX
DT 26-FEB-2002 (first entry)
XX
DE TRA-8 heavy chain.
XX
KW Tumour necrosis factor-related apoptosis-inducing ligand receptor;
KW TRAIL; TRAIL receptor DR5; cytosolic; apoptosis; cell proliferation;
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
XX
OS Mus musculus.
XX
PN WO200183560-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14151.
XX
PR 02-MAY-2000; 2000US-201344P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX
DR WPI: 2002-049338/06.
XX
PT Novel antibody specific for tumour necrosis factor-related
PT apoptosis-inducing ligand, useful for inhibiting cell proliferation in
PT cancer -
XX
PS Claim 26; Page 198-199; 229pp; English.
XX
CC The invention describes a novel antibody which recognizes a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
CC activity to a cell expressing DR5 in vivo. It is also useful for
CC preparing a therapeutic for selective apoptosis of abnormal or

PR 17-MAR-1994: 94EP-0104160.
 XX (MERE) MERCK PATENT GMBH.
 XX
 PI Adan J, Ansell KH, Bendig MM, Blasco F, Guessow D;
 PI Kettleborough AC, Mcljans F, Plutals J, Rosell E;
 XX WPI: 1995-336972/43.
 DR
 PT Anti-EGFR antibodies and single chain Fv antibody fragments -
 PT obtained from phage-antibody libraries, useful for diagnosis and
 PT therapy of tumours
 XX
 PS Disclosure: Figure 1A; 93pp: English.
 XX
 CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies
 CC and antibodies constructed from anti-EGFR antibody fragments can be
 CC used for diagnosis of tumours and assessment of tumour growth in
 CC vitro and in vivo. They may also be used in a pharmaceutical
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
 CC The antibodies and fragments are derived from mice but are humanised
 CC so as to cause minimum reaction against them. They are produced
 CC using the phage antibody library. (See AAT04011-T04026 and
 CC AAR79858-R79873)
 CC
 XX Sequence 119 AA:
 SQ
 Query Match 81.1%; Score 513.5; DB 16; Length 119;
 Best Local Similarity 84.9%; Pred. No. 1.7e-40;
 Matches 101; Conservative 5; Mismatches 12; Indels 1; Gaps 1;
 OY 1 OVQLOESGGGLVKGPGSLKLSCAASGFTPSDYVMVWVROTPEKRLFWATISDGSYTY 60
 DB 1 QVKLOESGGDLVKGPGSLKLSCAASGFTPSDYVMVWVROTPEKRLFWATISDGSYTY 60
 OY 61 PSDVKGRTTISRDNKNNLTLMSSLSKSEDTAMVYCSRYRD-DAMDYGGGTTTVSS 118
 DB 61 PSDVKGRTTISRDNKNNLTLMSSLSKSEDTAMVYCARLETGDYALDYGGGTTTVSS 119

RESULT 12
 AAM29994
 ID AAM29994; standard; protein; 119 AA.
 XX
 AC AAM29994;
 XX
 DT 12-MAR-1998 (first entry)
 XX
 DE Heavy chain variable region of MAb for t1A.
 XX
 DE Heavy chain variable region of monoclonal antibody; human; CD6; murine;
 KW leukocyte differentiation antigen; hybridoma; humanisation; mutagenesis;
 KW PCR; primer: amplification; inflammatory infiltration; skin; psoriasis;
 KW diagnosis.
 XX
 OS Mus sp.
 OS
 XX WO9719111-A2.
 XX
 PD 29-MAY-1997.
 XX
 PD 18-NOV-1996; 96MO-CU00004.
 XX
 PF 17-NOV-1995; 95CU-0000120.
 XX
 PR (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
 XX
 PA Lombardero Valladares J, Montero Casimiro JE, Perez Rodriguez R;
 PI Sierra Blazquez P, Tormo Bravo BR;
 XX WPI: 1997-298060/27.
 DR
 XX Monoclonal antibody against human CD6 antigen - useful for diagnosis

PT and treatment of psoriasis
 XX
 PS Claim 3; Page 27; 36pp; Spanish.
 XX
 CC This is the amino acid sequence of the heavy chain variable region
 CC of the monoclonal antibody (MAb) for t1A which recognises the human
 CC leukocyte differentiation antigen CD6. The MAb is a murine IgG2-type
 CC Ab produced by the usual hybridoma techniques. The coding sequence
 CC for the variable region can be used to generate humanised variants,
 CC especially by mutagenic PCR. CD6 has been shown to be expressed in
 CC T lymphocytes involved in the inflammatory infiltration of the skin
 CC in psoriasis. The anti-CD6 MAb can therefore be used to diagnose and
 CC treat psoriasis.
 CC
 XX Sequence 119 AA:
 SQ
 Query Match 81.1%; Score 513.5; DB 18; Length 119;
 Best Local Similarity 84.0%; Pred. No. 1.7e-40;
 Matches 100; Conservative 4; Mismatches 14; Indels 1; Gaps 1;
 OY 1 OVQLOESGGGLVKGPGSLKLSCAASGFTPSDYVMVWVROTPEKRLFWATISDGSYTY 60
 DB 1 EVQLVESGGGLVKGPGSLKLSCAASGFKFSRYAMSVWVROTPEKRLFWATISDGSYTY 60
 OY 61 PSDVKGRTTISRDNKNNLTLMSSLSKSEDTAMVYCSRYRD-DAMDYGGGTTTVSS 118
 DB 61 PSDVKGRTTISRDNKNNLTLMSSLSKSEDTAMVYCARLDYDIDYDSWGGGTTTVSS 119

RESULT 13
 AAR79161
 ID AAR79161; standard; peptide; 118 AA.
 XX
 AC AAR79161;
 XX
 DT 04-MAR-1996 (first entry)
 XX
 DE Human IgE receptor-binding antibody-related peptide heavy chain.
 XX
 KW Immunoglobulin E; antibody; receptor; monoclonal; detection;
 KW complementarity determining region.
 XX
 OS Mus sp.
 OS
 XX Key Location/Qualifiers
 FH 29..33
 FT Region /label= CDR1H
 FT /note= "all CDR regions are claimed"
 FT Region 48..64
 FT /label= CDR2H
 FT /note= "all CDR regions are claimed"
 FT Region 97..107
 FT /label= CDR3H
 FT /note= "all CDR regions are claimed"
 XX
 PN JP07165799-A.
 XX
 PD 27-JUN-1995.
 XX
 PD 22-OCT-1993; 93UP-0264792.
 XX
 PF 22-OCT-1993; 93UP-0264792.
 XX
 PR (ASAK) ASAKI BREWERIES LTD.
 XX
 PA (NIKK-) NIKKA WHISKY KK.
 PA (TORI) TORII YAHUKIN KK.
 PA (TSUR/) TSURA T.
 XX
 DR WPI: 1995-261292/34.
 DR N-PSDB: AAO96288.
 XX
 PT Novel monoclonal antibody against human high-affinity IgE receptor -
 PT and DNA fragment encoding the MAb, for the specific identification

PT of human Fc-epsilon RI
 XX
 PS Claim 9; Page 16; 20pp; Japanese.
 XX
 CC Polypeptides which specifically recognise human IgE receptor (Fc-
 CC epsilon-RI) have been isolated and sequenced. The new peptides are
 CC related to a monoclonal antibody against Fc-epsilon-RI and are
 CC either heavy or light chain molecules. The heavy chain molecules
 CC have the general formula FRI-CDRIH-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.
 CC to AAR79153, AAR79155, AAR79157, AAR79159 and AAR79161) and are encoded
 CC by AAO96280, AAO96282, AAO96284, AAO96286 and AAO96288. FRI is a
 CC polypeptide having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide,
 CC FR3 is a 33-35aa polypeptide and FR4 is a 12-14 aa polypeptide.
 CC Similarly the light chains have the general formula
 CC FR5-CDRLH-FR6-CDRL2-FR7-CDRL3-FR8, (corresp. to AAR79154, AAR79156,
 CC AAR79158, AAR79160 and AAR79162) and are encoded by AAO96281, AAO96283,
 CC AAO96285, AAO96287 and AAO96289. FR5 is a 23-28 aa polypeptide, FR6 is a
 CC 14-16 aa polypeptide, FR7 is a 30-34 aa polypeptide and FR8 is a 9-11 aa
 CC polypeptide. All the peptides are derived from mouse hybridoma cells and
 CC are useful in the detection of the human Fc-epsilon-RI or for the
 CC elucidation of an antigen recognising region of a monoclonal antibody
 CC against human Fc-epsilon-RI.
 XX
 SQ Sequence 118 AA;
 Query Match 81.0%; Score 513; DB 16; Length 118;
 Best Local Similarity 82.5%; Pred. No. 1.9e-40;
 Matches 99; Conservative 8; Mismatches 9; Indels 4; Gaps 2;
 QY 1 QVQLQESGGGLVPRGSGSLKSCAASGFTFSDIYMWVRQPEKRLKLVNATISDGGSTYY 60
 DB 1 QVQLQESGGGLVPRGSGSLKSCAASGFTFSDIYMWVRQPEKRLKLVNATISDGGSTYY 58
 QY 61 PDSVKGRTISRDNKAKNTLQMSLSKSEPTAMVYCSR--YRYDAMDYWGQTTVYSS 118
 DB 59 PDYVKGRTISRDNKAKNTLQMSLSKSEPTAMVYCARNGTRIGYAVDYWGQTTVYSS 118
 RESULT 14
 AAR79887
 ID AAR79887 standard; Protein; 119 AA.
 AC AAR79887;
 XX
 DT 02-JUL-1996 (first entry)
 XX
 DE Anti-EGFR antibody heavy chain variable region (Clone S4 10H).
 XX
 KW Single chain antibody; antibody; epidermal growth factor receptor;
 KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
 KW assessment; phage antibody library.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..30
 FT /label= Framework region 1.
 FT Region 31..35
 FT /label= CDR1.
 FT Region 36..49
 FT /label= Framework region 2.
 FT Region 50..66
 FT /label= CDR2.
 FT Region 67..98
 FT /label= Framework region 3.
 FT Region 99..108
 FT /label= CDR3.
 FT Region 109..119
 FT /label= Framework region 4.
 PN W09525167-A1.
 XX
 XX 21-SEP-1995.

XX
 PF 16-MAR-1995; 95WO-EP00978.
 XX
 PR 02-DEC-1994; 94EP-0118970.
 PR 17-MAR-1994; 94EP-0104160.
 XX
 PA (MERE) MERCK PATENT GMBH.
 PI Aaan J, Ansell KH, Bendig MM, Biasco F, Guessow D;
 PI Kettleborough AC, Miltjans F, Piuats J, Rosell E;
 XX
 DR WPI; 1995-336972/43.
 XX
 PT Anti-EGFR antibodies and single chain Fv antibody fragments
 PT obtained from phage-antibody libraries, useful for diagnosis and
 PT therapy of tumours
 XX
 PS Disclosure; Figure 1B; 93pp; English.
 XX
 CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies
 CC and antibodies constructed from anti-EGFR antibody fragments can be
 CC used for diagnosis of tumours and assessment of tumour growth in
 CC vitro and in vivo. They may also be used in a pharmaceutical
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
 CC The antibodies and fragments are derived from mice but are humanised
 CC so as to cause minimum reaction against them. They are produced
 CC using the phage antibody library. (See AAT04011-T04026 and
 CC AAR79858-R79873)
 XX
 SQ Sequence 119 AA;
 Query Match 80.6%; Score 510.5; DB 16; Length 119;
 Best Local Similarity 84.0%; Pred. No. 3.3e-40;
 Matches 100; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
 QY 1 QVQLQESGGGLVPRGSGSLKSCAASGFTFSDIYMWVRQPEKRLKLVNATISDGGSTYY 60
 DB 1 EVKLQESGGLVPRGSGSLKSCAASGFTFSYGSWVRQPEKRLKLVNATISDGGSTYY 60
 QY 61 PDSVKGRTISRDNKAKNTLQMSLSKSEPTAMVYCSRYDD-AMDYWGQTTVYSS 118
 DB 61 PDYVKGRTISRDNKAKNTLQMSLSKSEPTAMVYCARLETGDAIDYWGQTTVYSS 119
 RESULT 15
 AAY32404
 ID AAY32404 standard; Protein; 138 AA.
 AC AAY32404;
 XX
 DT 13-MAR-2000 (first entry)
 XX
 DE Mouse anti-verotoxin II antibody Vtm1-1 heavy chain variable region.
 XX
 KW Verotoxin II; VT2; shiga-like toxin; Vtm1-1; MuVtm1-1;
 KW monoclonal antibody; heavy chain; mouse; humanised antibody;
 KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
 KW HUS; therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "signal peptide"
 FT Protein 20..138
 FT /note= "mature protein"
 FT Region 50..54
 FT /note= "complementarity determining region 1"
 FT Region 59..85
 FT /note= "complementarity determining region 2"
 FT Region 118..127
 FT /note= "complementarity determining region 3"
 XX

PN	MO9595629-A1.
XX	
PD	25-NOV-1999.
XX	
PF	19-MAY-1999; 99WO-US11179.
XX	
PR	20-MAY-1998; 98US-0086570.
XX	
PA	(TEIJ) TEIJIN LTD.
PA	(PROF-) PROTEIN DESIGN LABS INC.
PI	
XX	
PI	Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
XX	
DR	WPI: 2000-086580/07.
DR	N-PDBE: AA235241.
XX	
PT	Humanized antibody binding to verotoxin II used for treating Verotoxin
PT	producing E. coli -
XX	
PS	Claim 5; Fig 1b; 59pp; English.
XX	

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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:09:39 : Search time 24.3478 Seconds
(without alignments)
947.817 Million cell updates/sec

Title: US-09-144-886-87

Perfect score: 586

Sequence: 1 DIELTQSPASLAVSLGQRAT.....QQSNEDPFTFGSGTKLEIKR 112

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	80.4	111	11	Q920E9 mus musculus
2	439	74.9	103	11	Q9180 mus musculus
3	386	65.9	108	4	Q9UL77 homo sapien
4	383	65.4	108	4	Q9UL70 homo sapien
5	380.5	64.9	107	4	Q96SA9 homo sapien
6	377.5	64.4	238	11	Q99M37 mus musculus
7	375.5	64.1	109	4	Q9UL78 homo sapien
8	370	63.1	214	11	Q9RIAS mus musculus
9	369.5	63.1	107	4	Q9UL81 homo sapien
10	367	62.6	108	4	Q9UL83 homo sapien
11	366.5	62.5	238	11	Q9VC16 mus musculus
12	365	62.3	234	11	Q91WF8 mus musculus
13	362	61.8	108	4	Q9UL79 homo sapien
14	357.5	61.0	239	11	Q8VCD0 mus musculus
15	357.5	61.0	239	11	Q8VC55 mus musculus
16	356	60.8	234	11	Q8R062 mus musculus

17	351.5	60.0	109	4	Q9UL85 mus musculus
18	351	59.9	234	11	Q8VCP0 mus musculus
19	350	59.7	114	4	Q9UL80 mus musculus
20	349.5	59.6	119	4	Q9UL86 mus musculus
21	345	58.9	298	11	Q9QYF0 mus musculus
22	342	58.4	107	11	Q9ER29 mus musculus
23	342	58.4	233	11	Q91WS9 mus musculus
24	340.5	58.1	106	5	Q9U410 schistosoma
25	339	57.8	109	11	Q920E6 mus musculus
26	338.5	57.8	104	11	Q8VDP0 mus musculus
27	336.5	57.4	104	11	Q9JL82 mus musculus
28	333	56.8	108	11	Q8VIT0 mus musculus
29	330	56.3	116	4	Q96PF6 mus musculus
30	329	56.1	101	11	Q9JL78 mus musculus
31	327	55.8	234	11	Q8R028 mus musculus
32	319.5	54.5	235	11	Q91W12 mus musculus
33	316	53.9	97	11	Q9JL76 mus musculus
34	316	53.9	99	11	Q9JL74 mus musculus
35	315	53.8	107	11	Q9JL84 mus musculus
36	313	53.4	218	11	Q92551 mus musculus
37	300.5	51.3	241	11	Q921A6 mus musculus
38	300	51.2	127	11	Q92359 mus musculus
39	289	49.3	109	6	Q9N0W5 oryctolagus
40	255.5	43.6	233	4	Q8YBC9 mus musculus
41	238.5	40.7	107	4	Q9NSD6 mus musculus
42	236.5	40.3	107	4	Q9UL82 mus musculus
43	235.5	40.2	237	4	Q8WUK4 mus musculus
44	234.5	40.0	237	4	Q8WTU6 mus musculus
45	220.5	37.6	110	4	Q8TE63 mus musculus

ALIGNMENTS

RESULT 1					
ID	Q920E9	PRELIMINARY:	PRT:	111	AA.
AC	Q920E9:				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE	Pterin-mimicking anti-Idiotope kappa chain variable region (fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Atkin J.D., Tape A., Jennings I.G., Horvath O., Cotton R.G.H.;				
RT	"Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."				
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF307935; AAL09419.1; -				
DR	InterPro; IPR003006; I9_MHC.				
DR	Pfam; PF00047; I9; 1.				
FT	NON_TER	1			
FT	NON_TER	111			
SQ	SEQUENCE	111	AA;	12046	MM; 1E46988AA6858526 CRC64;
Query Match		80.4%;	Score 471;	DB 11;	Length 111;
Best Local Similarity		81.1%;	Pred. No. 1.9e-45;		
Matches	90;	Conservative	8;	Mismatches	13;
				Indels	0;
				Gaps	0;
Qy	1	DIELTQSPASLAVSLGQRATISGRASEVDSYGSFWMYQKRGQPKLLIYRASNLDP	60		
Db	1	DIELTQSPASLAVSLGQRATISGRASEVDSYGSFWMYQKRGQPKLLIYRASNLDP	60		
Qy	61	GIPARSSGSGSDPTLTINPVEADVATYYCQSNEDPFTFGSGTKLEIK	111		
Db	61	GIPARSSGSGSDPTLTINPVEADVATYYCQSNEDPFTFGSGTKLEIK	111		

```

RESULT 2
O9UL80
ID O9UL80 PRELIMINARY: PRT: 103 AA.
AC O9UL80;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
   (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL: AF206026; AAF69324.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AB21 CRC64;

Query Match
Best Local Similarity 74.9%; Score 439; DB 11; Length 103;
Matches 83; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

OY 9 ASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGQPKLLIYRASNEPGIPARFSG 68
DB 1 ASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGQPKLLIYRASNEPGIPARFSG 60
OY 69 SSGGTDETLTINVEADVAITYCOOSNEDPTFGSGTKLEIK 111
DB 61 SSGGTDETLTINVEADVAITYCOOSNEDPTFGSGTKLEIK 103

RESULT 3
O9UL77
ID O9UL77 PRELIMINARY: PRT: 108 AA.
AC O9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035037; AAD56273.1; -.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 1

```

```

FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716CAD16F3 CRC64;

Query Match
Best Local Similarity 65.9%; Score 386; DB 4; Length 108;
Matches 71; Conservative 20; Mismatches 17; Indels 4; Gaps 1;

OY 1 DIELTQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGQPKLLIYRASNEPG 60
DB 1 DIELTQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGQPKLLIYRASNEPG 56
OY 61 GIPARFSGSGGTDETLTINVEADVAITYCOOSNEDPTFGSGTKLEIKR 112
DB 57 GIPARFSGSGGTDETLTINVEADVAITYCOOSNEDPTFGSGTKLEIKR 108

RESULT 4
O9UL70
ID O9UL70 PRELIMINARY: PRT: 108 AA.
AC O9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035044; AAD56280.1; -.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match
Best Local Similarity 65.4%; Score 383; DB 4; Length 108;
Matches 71; Conservative 19; Mismatches 18; Indels 4; Gaps 1;

OY 1 DIELTQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGQPKLLIYRASNEPG 60
DB 1 DIELTQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGQPKLLIYRASNEPG 56
OY 61 GIPARFSGSGGTDETLTINVEADVAITYCOOSNEDPTFGSGTKLEIKR 112
DB 57 GIPARFSGSGGTDETLTINVEADVAITYCOOSNEDPTFGSGTKLEIKR 108

RESULT 5
O96SA9
ID O96SA9 PRELIMINARY: PRT: 107 AA.
AC O96SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
   variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

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RESULT 6
ID Q99M37 PRELIMINARY: PRT: 238 AA.
AC Q99M37: 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL: U96396; AAB68785.1; -
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 64.9%; Score 380.5; DB 4; Length 107;
Best Local Similarity 64.3%; Pred. No. 2.9e-35;
Matches 72; Conservative 19; Mismatches 16; Indels 5; Gaps 2;

OY 1 DIELTOSPASLAVSLGQRTATISCRASESDYSGHSMQWYQKPGQPKLLIYRASNLKP 60
DB 1 DIELTOSPASLAVSLGQRTATISCRASESDYSGHSMQWYQKPGQPKLLIYRASNLKP 60
OY 61 GIPARFSGSGGDTFTLTINPEADVATYYCOQSNEDPFTGSGTKLEIKR 112
DB 57 GIPARFSGSGGDTFTLTINPEADVATYYCOQSNEDPFTGSGTKLEIKR 107

RESULT 7
ID Q9UL78 PRELIMINARY: PRT: 109 AA.
AC Q9UL78: 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035036; AAD56272.1; -
DR HSP: P80362; IWTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 64.1%; Score 375.5; DB 4; Length 109;
Best Local Similarity 65.2%; Pred. No. 1.1e-34;
Matches 73; Conservative 15; Mismatches 21; Indels 3; Gaps 1;

OY 1 DIELTOSPASLAVSLGQRTATISCRASESDYSGHSMQWYQKPGQPKLLIYRASNLKP 60
DB 1 EIVLTOSPTSLSPERATLSRNASQSVS---SYLAWYQKPGQAPRLIYAGASRRAT 57
OY 61 GIPARFSGSGGDTFTLTINPEADVATYYCOQSNEDPFTGSGTKLEIKR 112
DB 58 GIPARFSGSGGDTFTLTINPEADVATYYCOQSNEDPFTGSGTKLEIKR 109

RESULT 8
ID Q9RIAS PRELIMINARY: PRT: 214 AA.
AC Q9RIAS: 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE Kappa light chain of Mab7 (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv)."
RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF152371; AAD40242.1; -
DR HSP: P01679; 2FBJ.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00406; IgV_1.
DR SMART: SM00410; IG_Like_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1

Query Match 64.4%; Score 377.5; DB 11; Length 238;
Best Local Similarity 63.7%; Pred. No. 1.8e-34;
Matches 72; Conservative 19; Mismatches 21; Indels 1; Gaps 1;

OY 1 DIELTOSPASLAVSLGQRTATISCRASESDYSGHSMQWYQKPGQPKLLIYRASNLKP 59
DB 20 DVMVTQTPSLVSLGDPASISCRSSQSIHNSNGNTYLEMYLQKPGSKLLIYKVSNNP 79
OY 60 PCIPARFSGSGGDTFTLTINPEADVATYYCOQSNEDPFTGSGTKLEIKR 112
DB 80 SCVPDRFSGSGGDTFTLTINPEADVATYYCOQSNEDPFTGSGTKLEIKR 132

[illegible]

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FN [1]
RP SEQUENCE FROM N.A..
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Wysin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HMBL; AF035031; AAD56267.1; -.
DR HSSP; P80362; 1MTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 108
SO SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA6EEA CRC64;

Query Match.
Match Local Similarity 62.6%; Score 367; DB 4; Length 108;
Matches 72; Conservative 16; Mismatches 20; Indels 4; Gaps 1

OY 1 DIETLOSPASIAVSIGQATTCISCRASESVSDSGHSFMOWOOKPGOPKLLIYRASNLKP 60
   :|::|||::||| |::|||::|||::||| | ::|||::|||::|||::||| |
Db 1 EIVMWQSPATLSVSGERATLISCRAOSVSN---LANYYOKPGQAPRLLIYCASTRAT 56
   1 GIPARFGSGGTDFTLTINPEADVATVYCOQSENDPFETFGSGCTKLEIKR 112
   1 GIPAFSSGSGSTETTLTITSLQGFEDPAVYVOHNNMPTGTGGPGTKVDIKR 108

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[illegible]

RESULT 12
Q91WF8 PRELIMINARY: PRT: 234 AA.
AC Q91WF8:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DR 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC015292; AAH15292.1; -
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001865; Ribosomal_S2.
DR Pfam: PF00047; Ig_2.
DR PROSITE: PS00290; Ig_MHC; UNKNOWN_1.
DR PROSITE: PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 62.3%; Score 365; DB 11; Length 234;
Best Local Similarity 60.7%; Pred. No. 4.5e-33;
Matches 68; Conservative 19; Mismatches 21; Indels 4; Gaps 1;

QY 1 DIELTOSPASLAVSLGQRATISGRASESVDSYGHSMQYQKPGQPKLLIYRASNLPP 60
DB 21 DIQMTOTTSLSASLQDRVTISCRASQDISNTR---LNNYQKAPDGTVKLLIYTSRLYL 76
QY 61 GIPARFSGSGGDTFTLTINPYEADVDVATYYCQSNEDPFTFGSGTKLEIKR 112
DB 77 GVPFRFSGSGGDTFTLTINPYEADVDVATYYCQSNEDPFTFGSGTKLEIKR 128

RESULT 13

Q9UL79 PRELIMINARY: PRT: 108 AA.
AC Q9UL79:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP: P01607; IRET.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 61.8%; Score 362; DB 4; Length 108;
Best Local Similarity 61.6%; Pred. No. 3.6e-33;

Matches 69; Conservative 17; Mismatches 22; Indels 4; Gaps 1;

QY 1 DIELTOSPASLAVSLGQRATISGRASESVDSYGHSMQYQKPGQPKLLIYRASNLPP 60
DB 1 DIQMTOTTSLSASLQDRVTISCRASQDISNTR---LNNYQKAPDGTVKLLIYTSRLYL 76
QY 61 GIPARFSGSGGDTFTLTINPYEADVDVATYYCQSNEDPFTFGSGTKLEIKR 112
DB 57 GVPFRFSGSGGDTFTLTINPYEADVDVATYYCQSNEDPFTFGSGTKLEIKR 108

RESULT 14

Q8TCD0 PRELIMINARY: PRT: 239 AA.
AC Q8TCD0:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC022362; AAH22362.1; -
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 61.0%; Score 357.5; DB 4; Length 239;

Best Local Similarity 60.2%; Pred. No. 3.2e-32;
Matches 68; Conservative 19; Mismatches 25; Indels 1; Gaps 1;

QY 1 DIELTOSPASLAVSLGQRATISGRASESVDSYGHSMQYQKPGQPKLLIYRASNLPP 59
DB 21 DVMTOSPLSLPYLQGPASISCRSTQSLVSYSGNTLYLNMFGQRPQSPRRLLIYKSNND 80
QY 60 PGIPARFSGSGGDTFTLTINPYEADVDVATYYCQSNEDPFTFGSGTKLEIKR 112
DB 81 SGVPRFSGSGGDTFTLTINPYEADVDVATYYCQSNEDPFTFGSGTKLEIKR 133

RESULT 15

Q8VC55 PRELIMINARY: PRT: 239 AA.
AC Q8VC55:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC021781; AAH21781.1; -
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00409; Ig_2.
DR SMART: SM00407; IGC1; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00290; Ig_MHC; UNKNOWN_1.
KW Hypothetical protein.

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Page 6

SQ SEQUENCE 239 AA; 26303 MW; C16119CACCA25C337 CRC64;

Query Match	61.08;	Score 357.5;	DB 11;	Length 239;
Best Local Similarity	60.28;	Pred No 3	2a-32.	

Matches 68; Conservative 21; Mismatches 23; Indels 1; Gaps 1;

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OY      1 DIETQSPASLAVSLGQRTATISCRASES-VDSYGHFQMOWYQKPGQPKLLIRASNLE 59
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      21 DVLITQTPLSFVNIGQASISCKSTKSLNSDGFYIWDWYIQKPGQSPQLLIIVSNRF 80

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Qy 60 PGIPARFGSGSGDTFTLTINPVEADVAITYCCQSNEDPFTFGSGTKLEIKR 112
:::|||||:::|:::|:::|:::|
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYCFSQHNPHTYTFGGGTKEIKR 133

Db 21 DVVLQTPLSPVNIQDQASISCKSTKSLNSDGFYLLDWYLQKPGQSPQLLYLVSNRF 80

60 PGIPARFSGSGSGLDTLTINPVEADDAVATYYCQSQSNEDPFTFGSGTKLEIKR 112

Db 81 SGVPDRFSSGGSGDTFLKISRVEADLGVIYCFQSNHLPYTFGGGIRKLEIKR 133

Search completed: January 13, 2003, 15:12:38
Job time : 25.3478 secs

Job time : 25.3478 secs

GenCore version 5.1.3
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OW protein - protein search, using sw model

Run on: January 13, 2003, 15:11:24 : Search time 7.7913 Seconds
(without alignments)
278.890 Million cell updates/sec

Title: US-09-144-886-87
Perfect score: 586
Sequence: 1 DIETQSPASLAVSLGORAT.....QOSNEDPFTGSGTKLEIKR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : Published_Applications_MA:
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2: /cgn2_6/ptodata/1/pubpaa/PCIT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586	100.0	112	9	US-09-144-886-87
2	545	93.0	112	9	US-09-144-886-81
3	540	92.2	112	10	US-09-810-502-37
4	537	91.6	112	9	US-09-144-886-86
5	534	91.1	112	9	US-09-144-886-86
6	531	90.6	112	9	US-09-144-886-84
7	527	89.9	112	9	US-09-144-886-85
8	518	88.4	134	10	US-09-881-823-2
9	511	87.2	112	9	US-09-144-886-94
10	507	86.5	112	10	US-09-810-502-36
11	491	83.8	238	9	US-09-903-327A-4
12	489	83.4	132	9	US-09-879-461-2
13	477	81.4	112	9	US-09-144-886-95
14	476	81.2	106	10	US-09-802-077-6
15	476	81.2	106	10	US-09-802-096-6
16	464	79.0	269	12	US-10-027-770-2
17	463	79.0	269	12	US-10-027-770-5
18	461.5	78.8	111	9	US-09-144-886-93
19	461	78.7	131	10	US-09-286-240-2

20	460	78.5	131	9	US-09-879-461-58	Sequence 58, Appl
21	459	78.3	129	10	US-09-839-447A-2	Sequence 2, Appl
22	456	77.8	111	10	US-09-920-171-5	Sequence 5, Appl
23	454	77.5	131	9	US-09-879-461-14	Sequence 14, Appl
24	452	77.1	111	10	US-09-802-077-2	Sequence 2, Appl
25	452	77.1	111	10	US-09-802-096-2	Sequence 2, Appl
26	443	75.6	218	10	US-09-917-410-2	Sequence 2, Appl
27	440.5	75.2	110	9	US-09-974-052-13	Sequence 13, Appl
28	440.5	75.2	110	9	US-09-974-051-13	Sequence 13, Appl
29	436	74.4	114	10	US-09-920-171-10	Sequence 10, Appl
30	436	74.4	218	10	US-09-802-077-9	Sequence 9, Appl
31	436	74.4	218	10	US-09-802-096-9	Sequence 9, Appl
32	436	74.4	218	10	US-09-920-171-13	Sequence 13, Appl
33	434	74.1	114	10	US-09-920-171-9	Sequence 9, Appl
34	431	73.5	111	10	US-09-920-171-6	Sequence 6, Appl
35	430	73.4	114	10	US-09-920-171-8	Sequence 8, Appl
36	430	73.4	218	10	US-09-920-171-15	Sequence 15, Appl
37	430	73.4	218	10	US-09-920-171-17	Sequence 17, Appl
38	430	73.4	218	10	US-09-920-171-19	Sequence 19, Appl
39	430	73.4	218	10	US-09-920-171-24	Sequence 24, Appl
40	430	73.4	248	10	US-09-920-171-22	Sequence 22, Appl
41	430	73.4	248	10	US-09-920-171-23	Sequence 23, Appl
42	407	69.5	111	10	US-09-920-171-7	Sequence 7, Appl
43	399	68.1	112	9	US-09-144-886-89	Sequence 89, Appl
44	397	67.7	108	10	US-09-056-1608-12	Sequence 12, Appl
45	397	67.7	109	10	US-09-811-123-6	Sequence 6, Appl

ALIGNMENTS

```

RESULT 1
US-09-144-886-87
; Sequence 87, Application US/09144886
; Patent No. US2002015114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144.886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C25 region VL epitope 2
US-09-144-886-87

Query Match      100.0%  Score 586:  DB 9:  Length 112:
Best Local Similarity 100.0%:  Pred. No. 3.3e-37:
Matches 112:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

QY      1  DIETQSPASLAVSLGORATISCRASESVDSYGHSEFMWYQKPGQPPKLLYRASNLKP 60
        |||||||
DB       1  DIETQSPASLAVSLGORATISCRASESVDSYGHSEFMWYQKPGQPPKLLYRASNLKP 60
        |||||||

QY      61  GIPARFSGSGSTDTLTITNPVEADVATYYCOQSNEDPFTGSGTKLEIKR 112
        |||||||
DB       61  GIPARFSGSGSTDTLTITNPVEADVATYYCOQSNEDPFTGSGTKLEIKR 112
        |||||||

RESULT 2
US-09-144-886-81
; Sequence 81, Application US/09144886
; Patent No. US2002015114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D

```

APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 81
LENGTH: 112
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-81

Query Match 93.0%; Score 545; DB 9; Length 112;
Best Local Similarity 93.8%; Pred. No. 3,5e-34;
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIETGSPASLAVSLGQRATISCRASESDVSGHSPMOWYQKPGQPKLLIYRASNLSP 60
DB 1 DIETGSPASLAVSLGQRATISCRASESDVSGHSPMOWYQKPGQPKLLIYRASNLSP 60

QY 61 GIPARFSGSGSDFTLTINPVADVDVATYYCCQSNEDPFTFGSGTKLEIKR 112
DB 61 GIPARFSGSGSDFTLTINPVADVDVATYYCCQSNEDPFTFGSGTKLEIKR 112

RESULT 3
US-09-810-502-37
Sequence 37, Application US/09810502
Patent No. US20020034765A1
GENERAL INFORMATION:
APPLICANT: Padlan, Eduardo A.
Daugherty, Bruce L.
Mark, George E.
TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY
OF ANTIBODY VARIABLE DOMAINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/810,502
FILING DATE: 16-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/905,280
FILING DATE: 01-Aug-1997
APPLICATION NUMBER: 08/609,218
FILING DATE: 01-Mar-1996
APPLICATION NUMBER: 08/109,187
FILING DATE: 19-Aug-1993
APPLICATION NUMBER: 07/702,217
FILING DATE: 17-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18410CC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720

TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-810-502-37

Query Match 92.2%; Score 540; DB 10; Length 112;
Best Local Similarity 92.9%; Pred. No. 8,2e-34;
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIETGSPASLAVSLGQRATISCRASESDVSGHSPMOWYQKPGQPKLLIYRASNLSP 60
DB 1 DIETGSPASLAVSLGQRATISCRASESDVSGHSPMOWYQKPGQPKLLIYRASNLSP 60

QY 61 GIPARFSGSGSDFTLTINPVADVDVATYYCCQSNEDPFTFGSGTKLEIKR 112
DB 61 GIPARFSGSGSDFTLTINPVADVDVATYYCCQSNEDPFTFGSGTKLEIKR 112

RESULT 4
US-09-144-886-80
Sequence 80, Application US/09144886
Patent No. US2002015511A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 80
LENGTH: 112
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-80

Query Match 91.6%; Score 537; DB 9; Length 112;
Best Local Similarity 92.9%; Pred. No. 1,4e-33;
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIETGSPASLAVSLGQRATISCRASESDVSGHSPMOWYQKPGQPKLLIYRASNLSP 60
DB 1 DIETGSPASLAVSLGQRATISCRASESDVSGHSPMOWYQKPGQPKLLIYRASNLSP 60

QY 61 GIPARFSGSGSDFTLTINPVADVDVATYYCCQSNEDPFTFGSGTKLEIKR 112
DB 61 GIPARFSGSGSDFTLTINPVADVDVATYYCCQSNEDPFTFGSGTKLEIKR 112

RESULT 5
US-09-144-886-86
Sequence 86, Application US/09144886
Patent No. US2002015511A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98

; CURRENT FILING DATE: 1998-08-31
 ; NUMBER OF SEQ ID NOS: 98

SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 2B6 region VL epitope 3
US-09-144-886-94

Query Match
Best Local Similarity 87.2%; Score 511; DB 9; Length 112;
Matches 97; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 IEITQSPASLAVSLGQRATISCRASESYDSYSGHSPQWYQKPGQPKLLIYRASNLSP 61
DB 2 IEITQSPASLAVSLGQRATISCRASESYDSYSGHSPQWYQKPGQPKLLIYRASNLSP 61

QY 62 IPARFSGSGSGDTFTLTINPVEADVAITYCCQSNEDPFTFGSGTKLEIK 111
DB 62 VPARFSGSGSGDTFTLTINPVEADVAITYCCQSNEDPFTFGSGTKLEIK 111

RESULT 10
US-09-810-502-36
; Sequence 36, Application US/09810502
; Patent No. US20020034765A1
; GENERAL INFORMATION:
; APPLICANT: Padlan, Eduardo A.
; Daugherty, Bruce L.
; Mark, George E.
; TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY
; OF ANTIBODY VARIABLE DOMAINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/810, 502
; FILING DATE: 16-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/905,280
; FILING DATE: 01-Aug-1997
; APPLICATION NUMBER: 08/609,218
; FILING DATE: 01-Mar-1996
; APPLICATION NUMBER: 08/109,187
; FILING DATE: 19-Aug-1993
; APPLICATION NUMBER: 07/702,217
; FILING DATE: 17-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18410CC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3905
; TELEFAX: 732-594-4720
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-810-502-36

Query Match
Best Local Similarity 86.5%; Score 507; DB 10; Length 112;
Matches 98; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRATISCRASESYDSYSGHSPQWYQKPGQPKLLIYRASNLSP 60
DB 1 DIYTQSSNSLAVSLGERATISCRASESYDSYSGHSPQWYQKPGQPKLLIYRASNLSP 60

QY 61 GIPARFSGSGSGDTFTLTINPVEADVAITYCCQSNEDPFTFGSGTKLEIK 112
DB 61 GIPDRFSGSGSGDTFTLTISVEADVAITYCCQSNEDPFTFGSGTKLEIK 112

RESULT 11
US-09-903-327A-4
; Sequence 4, Application US/09903327A
; Patent No. US2002016433A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; Applicant: Li, Erquan
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-4

Query Match
Best Local Similarity 83.8%; Score 491; DB 9; Length 238;
Matches 94; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRATISCRASESYDSYSGHSPQWYQKPGQPKLLIYRASNLSP 60
DB 21 DIETQSPASLAVSLGQRATISCRASESYDSYSGHSPQWYQKPGQPKLLIYRASNLSP 80

QY 61 GIPARFSGSGSGDTFTLTINPVEADVAITYCCQSNEDPFTFGSGTKLEIK 112
DB 81 GIPARFSGSGSGDTFTLTINPVEADVAITYCCQSNEDPFTFGSGTKLEIK 132

RESULT 12
US-09-879-461-2
; Sequence 2, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; Gross, Mitchell S.
; Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; Swedeland Rd.
; CITY: King of Prussia

STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sulton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-879-461-2
Query Match 83.4%; Score 489; DB 9; Length 132;
Best Local Similarity 84.8%; Pred. No. 5.4e-30;
Matches 95; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
OY 1 DIETOSPASLAVSLGQRATISCRASESVDSYGHSMQWYQKPGOPKLLIYRASNLPP 60
DB 21 DIQLTQSPASLAVSLGQRATISCRASQSVYDGDYMMYQKPGOPKLLIYASNLSS 80
OY 61 GIPARFSGSGCTDFTLTINPEADDVATYYCOQSNEDPFTFGSGTKLEIKR 112
DB 81 GIPARFSGSGCTDFTLTINHPVEEDATYYCOQSNEDPFTFGSGTKLEIKR 132
RESULT 13
US-09-144-886-95
Sequence 95, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: P500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 95
LENGTH: 112
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-95
Query Match 81.4%; Score 477; DB 9; Length 112;
Best Local Similarity 81.2%; Pred. No. 3.6e-29;
Matches 91; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

OY 1 DIETOSPASLAVSLGQRATISCRASESVDSYGHSMQWYQKPGOPKLLIYRASNLPP 60
DB 1 DIETOSPASLAVSLGQRATISCRASESVYGTSLMQWYQKPGOPKLLIYASNLSS 60
OY 61 GIPARFSGSGCTDFTLTINPEADDVATYYCOQSNEDPFTFGSGTKLEIKR 112
DB 61 GIPARFSGSGCTDFTLTINHPVEEDATYYCOQSNEDPFTFGSGTKLEIKR 112
RESULT 14
US-09-802-077-6
Sequence 6, Application US/09802077
Patent No. US20010033842A1
GENERAL INFORMATION:
APPLICANT: Jardeu, Paula M.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: P0718P2C2US
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 6
LENGTH: 106
TYPE: PRT
ORGANISM: Mus musculus
US-09-802-077-6
Query Match 81.2%; Score 476; DB 10; Length 106;
Best Local Similarity 84.9%; Pred. No. 4e-29;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
OY 1 DIETOSPASLAVSLGQRATISCRASESVDSYGHSMQWYQKPGOPKLLIYRASNLPP 60
DB 1 DIQLTQSPASLAVSLGQRATISCRASQSVYDGDYMMYQKPGOPKLLIYASNLSS 60
OY 61 GIPARFSGSGCTDFTLTINPEADDVATYYCOQSNEDPFTFGSGT 106
DB 61 GIPARFSGSGCTDFTLTINHPVEEDATYYCOQSNEDPFTFGAGT 106
RESULT 15
US-09-802-096-6
Sequence 6, Application US/09802096
Patent No. US2001003839A1
GENERAL INFORMATION:
APPLICANT: Jardeu, Paula M.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
FILE REFERENCE: P0718P2C3US
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 6

; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-6

Query Match 81.2%; Score 476; DB 10; Length 106;
Best Local Similarity 84.9%; Pred. No. 4e-29;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGORATISGRASESYGHSFEMQWYQOKPGOPKLLIYRASNLTP 60
Db 1 DIETOSPASLAVSLGORATISGRASOSVDYDGDSTMMWYQOKPGOPKLLIYRASNLTP 60
QY 61 GIPARFSGSGSGTDFTLINPEADDVATYCCOQSNEDPFTFGSGT 106
Db 61 GIPARFSGSGSGTDFTLINHPVEEDATYCCOQSNEDPFTFGAGT 106

Search completed: January 13, 2003, 15:14:04
Job time : 7.7913 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:10:24 : Search time 11.2 Seconds
(without alignments)
294.229 Million cell updates/sec

Title: US-09-144-886-87

Perfect score: 586

Sequence: 1 DIELTQSPASLAVSLGQRAT.....QSNEDPFTGSGTKLEIKR 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents-AA:*

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525	89.6	131	1	US-08-137-117D-33
2	525	89.6	131	2	US-08-436-717-33
3	523	89.2	131	2	US-08-621-751A-10
4	522	89.1	149	2	US-08-894-922A-6
5	522	89.1	252	2	US-08-894-922A-14
6	522	89.1	271	2	US-08-894-922A-10
7	518	88.4	120	1	US-08-111-080-26
8	518	88.4	120	1	US-08-211-980-26
9	518	88.4	120	5	PCT-US93-07967-26
10	511	87.2	121	1	US-08-111-080-22
11	511	87.2	121	1	US-08-211-980-22
12	511	87.2	121	1	US-08-211-980-22
13	506	86.3	111	5	PCT-US93-07967-22
14	506	86.3	121	1	US-08-111-080-18
15	506	86.3	121	1	US-08-211-980-18
16	506	86.3	121	5	PCT-US92-07111-17
17	506	86.3	121	5	PCT-US93-07967-18
18	501	85.5	112	3	US-09-065-053-13
19	490	83.6	215	4	US-09-170-769A-4
20	489	83.4	132	2	US-08-483-636-2
21	489	83.4	132	2	US-08-483-636-2
22	481	82.1	111	1	US-08-491-845-8
23	479	81.7	131	4	US-08-579-378A-14
24	476	81.2	106	3	US-08-466-151-6
25	476	81.2	106	4	US-08-466-151-6
26	470	80.2	113	2	US-08-553-497A-6
27	468	79.9	113	2	US-08-553-497A-10

28	465	79.4	111	3	US-08-881-037-76	Sequence 76, Appl
29	464	79.2	106	4	US-09-170-769A-25	Sequence 25, Appl
30	464	79.2	131	1	US-08-137-117D-25	Sequence 25, Appl
31	464	79.2	131	2	US-08-436-717-25	Sequence 25, Appl
32	463	79.0	111	1	US-07-634-278-54	Sequence 54, Appl
33	463	79.0	111	1	US-08-477-728-54	Sequence 54, Appl
34	463	79.0	111	1	US-08-474-040-54	Sequence 54, Appl
35	463	79.0	111	1	US-08-487-200-54	Sequence 54, Appl
36	463	79.0	111	4	US-08-484-537-54	Sequence 54, Appl
37	463	79.0	131	1	US-07-634-278-67	Sequence 67, Appl
38	463	79.0	131	1	US-08-477-728-67	Sequence 67, Appl
39	463	79.0	131	1	US-08-474-040-67	Sequence 67, Appl
40	463	79.0	131	1	US-08-487-200-67	Sequence 67, Appl
41	463	79.0	131	2	US-08-621-751A-14	Sequence 14, Appl
42	463	79.0	131	4	US-08-484-537-67	Sequence 67, Appl
43	462	78.8	120	1	US-08-111-080-24	Sequence 24, Appl
44	462	78.8	120	1	US-08-211-980-24	Sequence 24, Appl
45	462	78.8	120	5	PCT-US93-07967-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-137-117D-33
; Sequence 33, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESS: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25, 258
; REFERENCE/DOCKET NUMBER: 53466/126/AOAK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid

RESULT 4
US-08-894-922A-6

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: Patent No. 5863765
: GENERAL INFORMATION:
: APPLICANT: BERRY, Mark John
: APPLICANT: DAVIS, Paul James
: APPLICANT: VAN DER LOOT, Cornelius P.E.
: APPLICANT: WHITELAM, Garry Clark
: TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
: STREET: 1100 New York Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: United States
: ZIP: 20005-3918
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS Word
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/894,922A
: FILING DATE: 03-SEP-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9504344.4
: FILING DATE: 03-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/GB96/00468
: FILING DATE: 01-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Kokulis, Paul K.
: REGISTRATION NUMBER: 16,773
: REFERENCE/DOCKET NUMBER: 60113/241261
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)-861-3503
: TELEFAX: (202)-822-0944
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 149 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-894-922A-6

Query Match      89.1%; Score 522; DB 2; Length 149;
Best Local Similarity 90.4%; Pred. No. 1.9e-42;
Matches 103; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

Oy      1 DIETQSPASLAVSISGQRTISCRASESVDSYGHSFMQWYQOKPGOPKLLIYRASNI 60
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      23 DIETQSPDSLAVSLGQRTISCRASESVDSYGHSFMQWYQOKPGOPKLLIYRASNES 82

Oy      61 GIPARFSGSGGTDTLTINPEADVATYYCOQSNEDP--FTFGSGTKLEIKR 112
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      83 GIPARFSGGTDTLTINPEADVATYYCOQSDERPYMTTFCGKLEIKR 136

RESULT 5
US-08-894-922A-14
: Sequence 14, Application US/08894922A
: Patent No. 5863765
: GENERAL INFORMATION:
: APPLICANT: BERRY, Mark John
: APPLICANT: DAVIS, Paul James
: APPLICANT: VAN DER LOOT, Cornelius P.E.
: APPLICANT: WHITELAM, Garry Clark
: TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
: STREET: 1100 New York Avenue, N.W.
: CITY: Washington
```

```
: STATE: D.C.
: COUNTRY: United States
: ZIP: 20005-3918
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS Word
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/894,922A
: FILING DATE: 03-SEP-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9504344.4
: FILING DATE: 03-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/GB96/00468
: FILING DATE: 01-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Kokulis, Paul K.
: REGISTRATION NUMBER: 16,773
: REFERENCE/DOCKET NUMBER: 60113/241261
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)-861-3503
: TELEFAX: (202)-822-0944
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 252 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-894-922A-14

Query Match      89.1%; Score 522; DB 2; Length 252;
Best Local Similarity 90.4%; Pred. No. 3.3e-42;
Matches 103; Conservative 4; Mismatches 5; Indels 2; Gaps 1;
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```
Oy      1 DIETQSPASLAVSISGQRTISCRASESVDSYGHSFMQWYQOKPGOPKLLIYRASNI 60
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      126 DIETQSPDSLAVSLGQRTISCRASESVDSYGHSFMQWYQOKPGOPKLLIYRASNES 185

Oy      61 GIPARFSGSGGTDTLTINPEADVATYYCOQSNEDP--FTFGSGTKLEIKR 112
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      186 GIPARFSGGTDTLTINPEADVATYYCOQSDERPYMTTFCGKLEIKR 239

RESULT 6
US-08-894-922A-10
: Sequence 10, Application US/08894922A
: Patent No. 5863765
: GENERAL INFORMATION:
: APPLICANT: BERRY, Mark John
: APPLICANT: DAVIS, Paul James
: APPLICANT: VAN DER LOOT, Cornelius P.E.
: APPLICANT: WHITELAM, Garry Clark
: TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
: STREET: 1100 New York Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: United States
: ZIP: 20005-3918
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS Word
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/894,922A
: FILING DATE: 03-SEP-1997
: CLASSIFICATION: 435
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FRAG

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9504344.4
FILING DATE: 03-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/00468
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kokulis, Paul K.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 60113/241261
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-861-3503
TELEFAX: (202)-822-0944
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-894-922A-10

Query Match 89.1%; Score 522; DB 2; Length 271;
Best Local Similarity 90.4%; Pred. No. 3.6e-42;
Matches 103; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 1 DIETQSPASLAVSLGQRATISCRASEVDYSGHSFQMWOYQKPGQPKLLIYRASNLKP 60
DB 145 DIETQSPASLAVSLGQRATISCRASEVDYSGHSFQMWOYQKPGQPKLLIYRASNLKS 204
QY 61 GIPARFSGSGGTDFLTINPYEADVDVATYYCOQSNEDP--FTFGSGTKLEIKR 112
DB 205 GIPARFSGSGGTDFLTINPYEADVDVATYYCOQSNEDPYMYTFGGTKLEIKR 258

RESULT 7
US-08-111-080-26
Sequence 26, Application 08/111080
Patent No. 5558865
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/111,080
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-111-080-26

Query Match 88.4%; Score 518; DB 1; Length 120;
Best Local Similarity 89.3%; Pred. No. 3.6e-42;
Matches 100; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRATISCRASEVDYSGHSFQMWOYQKPGQPKLLIYRASNLKP 60
DB 1 DIETQSPASLAVSLGQRATISCRASEVDYSGHSFQMWOYQKPGQPKLLIYRASNLKS 60

QY 61 GIPARFSGSGGTDFLTINPYEADVDVATYYCOQSNEDPFTFGSGTKLEIKR 112
DB 61 GIPARFSGSGGTDFLTINPYEADVDVATYYCOQSNKDKPLFTGAGTKLEIKR 112

RESULT 8
US-08-211-980-26
Sequence 26, Application US/08211980
Patent No. 5665569

GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,980
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-980-26

Query Match 88.4%; Score 518; DB 1; Length 120;
Best Local Similarity 89.3%; Pred. No. 3.6e-42;

Matches 100; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSMFYQOQKPGQPKLLIYRASNLKP 60
|||
Db 1 DIVLTQSPASLAVSLGQRTATISCRASESVDSYGHSMFYQOQKPGQPKLLIYRASNLKS 60

QY 61 GIPARFSSGSGTDFLTINPEADVAITYYCOQSNEDPFTGSGTKLEIKR 112
|||
Db 61 GIPARFSSGSGTDFLTINPEADVAITYYCOQSNKDPITFGAGTKLEIKR 112

RESULT 9
PCT-US93-07967-26
Sequence 26, Application PC/TUS9307967
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-07967-26

Query Match 88.4%; Score 518; DB 5; Length 120;
Best Local Similarity 89.3%; Pred. No. 3.6e-42;
Matches 100; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSMFYQOQKPGQPKLLIYRASNLKP 60
|||
Db 1 DIVLTQSPASLAVSLGQRTATISCRASESVDSYGHSMFYQOQKPGQPKLLIYRASNLKS 60

QY 61 GIPARFSSGSGTDFLTINPEADVAITYYCOQSNEDPFTGSGTKLEIKR 112
|||
Db 61 GIPARFSSGSGTDFLTINPEADVAITYYCOQSNKDPITFGAGTKLEIKR 112

RESULT 10
US-08-111-080-22
Sequence 22, Application 08/111080

Patent No. 5558665
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/111,080
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-111-080-22

Query Match 87.2%; Score 511; DB 1; Length 121;
Best Local Similarity 87.5%; Pred. No. 1.6e-41;
Matches 98; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSMFYQOQKPGQPKLLIYRASNLKP 60
|||
Db 1 DIVLTQSPASLAVSLGQRTATISCRASESVDSYGHSMFYQOQKPGQPKLLIYRASNLKS 60

QY 61 GIPARFSSGSGTDFLTINPEADVAITYYCOQSNEDPFTGSGTKLEIKR 112
|||
Db 61 GIPARFSSGSGTDFLTINPEADVAITYYCOQSNKDPITFGAGTKLEIKR 112

RESULT 11
US-08-211-980-22
Sequence 22, Application US/08211980
Patent No. 5665569
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago

STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,980
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO.: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-980-22

Query Match 87.2%; Score 511; DB 1; Length 121;
Best Local Similarity 87.5%; Pred. No. 1.6e-41;
Matches 98; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGGRATISCRASESDYSGHFMQWYQKPGPKLLIYRASNLEP 60
DB 1 DIYTOSPASLAVSLGGRATISCRASESDYSGHFMQWYQKPGPKLLIYVASNTLES 60
QY 61 GIPARFSGSGGTDFTLTINPEADDAVATYCCOQSNEDPPTFGSGTKLEIKR 112
DB 61 GVPARFSGSGSRDFTLTIDPVEADDAATYCCOQNNEDPLTFGAGTKLEIKR 112

RESULT 12
PCT-US93-07967-22
Sequence 22, Application PC/TUS9307967
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneoya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111

FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO.: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-07967-22

Query Match 87.2%; Score 511; DB 5; Length 121;
Best Local Similarity 87.5%; Pred. No. 1.6e-41;
Matches 98; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGGRATISCRASESDYSGHFMQWYQKPGPKLLIYRASNLEP 60
DB 1 DIYTOSPASLAVSLGGRATISCRASESDYSGHFMQWYQKPGPKLLIYVASNTLES 60
QY 61 GIPARFSGSGGTDFTLTINPEADDAVATYCCOQSNEDPPTFGSGTKLEIKR 112
DB 61 GVPARFSGSGSRDFTLTIDPVEADDAATYCCOQNNEDPLTFGAGTKLEIKR 112

RESULT 13
US-08-273-053-11
Sequence 11, Application US/08273053
Patent No. 5607847
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Recombinant human anti-human immunodeficiency
virus antibody.
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,053
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/01798
INFORMATION FOR SEQ. ID NO.: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-275-053-11

Query Match 86.3%; Score 506; DB 1; Length 111;
Best Local Similarity 87.4%; Pred. No. 4.5e-41;
Matches 97; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGGRATISCRASESDYSGHFMQWYQKPGPKLLIYRASNLEP 60
DB 1 DIYTOSPASLAVSLGGRATISCRASESDYSGHFMQWYQKPGPKLLIYVASNTLES 60
QY 61 GIPARFSGSGGTDFTLTINPEADDAVATYCCOQSNEDPPTFGSGTKLEIKR 111
DB 61 GVPARFSGSGSRDFTLTIDPVEADDAATYCCOQNNEDPLTFGAGTKLEIKR 111

```
RESULT 14
US-08-111-080-18
; Sequence 18, Application 08/111080
; Patent No. 5558865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3836
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-111-080-18

Query Match      86.3%; Score 506; DB 1; Length 121;
Best Local Similarity 86.6%; Pred. No. 4.9e-41;
Matches 97; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIETQSPASLAVSLGQRTATISCRASESVDSYSGHFMQYQKPGQOPRLIYRASNLKP 60
    |||||||
Db 1 DIVLTQSPASLAVSLGQRTATISCRASESVDSYSGHFMHYQKPGQSPRLIYVASNLKS 60
    |||||||

Qy 61 GIPARFSGSGSTDTLTINPVEADVAITYYCOQSNEDPFTGSGTKLEIKR 112
    |||||||
Db 61 GVPARFSGSGSRDFTLTIDPVEADDAITYYCOQNNEDPLAFGTGKLEIKR 112
    |||||||

RESULT 15
US-08-211-980-18
; Sequence 18, Application US/08211980
; Patent No. 5665569
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
```

```
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,980
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3836
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-980-18

Query Match      86.3%; Score 506; DB 1; Length 121;
Best Local Similarity 86.6%; Pred. No. 4.9e-41;
Matches 97; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIETQSPASLAVSLGQRTATISCRASESVDSYSGHFMQYQKPGQOPRLIYRASNLKP 60
    |||||||
Db 1 DIVLTQSPASLAVSLGQRTATISCRASESVDSYSGHFMHYQKPGQSPRLIYVASNLKS 60
    |||||||

Qy 61 GIPARFSGSGSTDTLTINPVEADVAITYYCOQSNEDPFTGSGTKLEIKR 112
    |||||||
Db 61 GVPARFSGSGSRDFTLTIDPVEADDAITYYCOQNNEDPLAFGTGKLEIKR 112
    |||||||
```

Search completed: January 13, 2003, 15:13:43
Job time : 12.2 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:07:08 ; Search time 30.1913 Seconds
(without alignments)
494.317 Million cell updates/sec

Title: US-09-144-886-87

Perfect score: 586

Sequence: 1 DIELQSPASLAVSLGQRAT.....QSNDEPFTFGSKLEIKR 112

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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2: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:*

3: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT:*

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6: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT:*

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13: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT:*

14: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT:*

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21: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*

22: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*

23: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	544	92.8	249	22	AA20436
2	543	92.7	112	22	AAU07480
3	543	92.7	112	22	AAU07516
4	543	92.7	252	22	AAU07497
5	540	92.2	112	12	AA13089
6	540	92.2	112	23	ABB77332
7	533	91.0	111	15	AAK47494
8	533	91.0	131	17	AAW01143
9	533	91.0	131	19	AAW4168
10	529	90.3	294	22	AA20442

11	529	90.3	732	22	AA20437
12	525	89.6	131	13	AA29008
13	525	89.6	325	22	AA20438
14	523	89.2	131	18	AAW30278
15	522	89.1	149	17	AAW02292
16	522	89.1	252	17	AAW02294
17	522	89.1	271	17	AAW02293
18	522	89.1	495	22	AA27414
19	521	88.9	249	22	AA20435
20	516	88.1	112	16	AA279158
21	515	87.9	120	15	AA48620
22	513	87.5	112	12	AA10539
23	511	87.2	121	17	AAW09259
24	510	87.0	110	15	AA20810
25	507	86.5	112	23	ABB77331
26	507	86.5	329	22	AA270840
27	506	86.3	111	16	AA265172
28	506	86.3	112	16	AA279156
29	506	86.3	121	17	AAW09274
30	502	85.7	113	22	AA271895
31	502	85.7	121	15	AA246615
32	501	85.5	112	17	AAW00830
33	501	85.5	112	18	AAW19016
34	501	85.5	112	18	AAW27358
35	499	85.2	121	15	AA246616
36	497	84.8	121	14	AA23346
37	495	84.5	132	12	AA210920
38	493.5	84.2	132	14	AA237716
39	493	84.1	107	18	AAW27353
40	493	84.1	112	18	AAW27527
41	493	84.1	237	20	AAW73873
42	493	84.1	240	20	AAW73875
43	493	84.1	260	16	AA277617
44	491	83.8	108	22	AAU07496
45	491	83.8	238	23	AA218371

ALIGNMENTS

RESULT 1	AA20436	standard; Protein; 249 AA.
ID	AA20436	
XX	21-JUN-2001	(first entry)
AC	AA20436	
XX	Anti-FIX/FIXa antibody 198/Al scfv.	
DT	Factor IX; FIX; Factor IXa; FIXa; scfv; antibody; procoagulant;	
XX	Factor VIII cofactor; blood coagulation disorder; haemophilia A;	
KW	haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.	
XX		
OS	Chimeric - Mus musculus.	
XX	Chimeric - Synthetic.	
FH	Key	Location/Qualifiers
FT	Protein	1..122
FT		/label= VH
FT	Region	99..111
FT		/label= CDR3
FT	Peptide	123..136
FT		/label= Linker
FT	Protein	137..249
FT		/label= VL
FT	Region	230..238
FT		/label= CDR3
FT	Misc-difference	142
FT		/note= "encoded by ACN"
FT	Misc-difference	224
FT		/note= "encoded by GCN"
FT		
XX		

Anti-FIX/FIXa anti
p64-k protein pro
Anti-FIX/FIXa anti
Light chain of Mm
FvKc-II VL region.
Yeast-FvKc-II-KEX2
FvKc-II-KEX2. Chi
Double-head anti
Anti-FIX/FIXa anti
Human Ige receptor
Sequence of the 11
Chimeric Mab 9.2.2
Monoclonal antibod
Light chain variab
Veneered 1B4 light
SNV-leader/hum
Murine NM-01 varia
Human Ige receptor
Mab NM-01 light ch
Monoclonal antibod
Sequence of the mo
Variable light cha
Anti-human FasL an
Light chain variab
Sequence of the mo
Sequence of the va
Kappa light chain
Mouse 4C10 anti-Id
Light chain variab
Light chain variab
Human antiFc epi1
Anti-C5 Mab N19/8
Synthetic antibody
Human penton base

PN WO200119992-A2.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-EP08936.
XX
PR 14-SEP-1999; 99AT-0001576.
XX
PA (BAXT) BAXTER AG.
XX
PI Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX
DR WPI; 2001-290358/30.
DR N-PSDB; AAF30726.
XX
PT New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
PS Example 10; Fig 17; 138pp; English.
XX
CC The present sequence is that of a single chain Fv (scFv) derivative
CC of antibody 198/A1, comprising the heavy (VH) and light (VL) chain
CC variable regions of 198/A1 joined by an artificial, flexible linker
CC peptide. The scFv was obtained by PCR amplification of cDNAs for
CC 198/A1 VH and VL regions and cloning in vector pDAP2. 198/A1 is
CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
CC antibodies of the invention. Anti-FIX/FIXa and their derivatives,
CC including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor
CC activity or FIXa activating activity. Administration leads to an
CC increase in the procoagulant activity of FIXa, even in the presence
CC of FVIIIa inhibitors. This allows for rapid blood coagulation even
CC in the absence of FVIII or FVIIIa, and in the case of FVIII
CC inhibitor patients. The antibodies and derivatives are used in a
CC claimed pharmaceutical composition for treating patients with blood
CC coagulation disorders, especially haemophilia A and haemorrhagic
CC diathesis.
XX
SQ Sequence 249 AA;
XX
Query Match 1 92.8%; Score 544; DB 22; Length 249;
Best Local Similarity 93.8%; Pred. No. 2.4e-39;
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
XX
QY 1 DIETQSPASLAVSLGQRATISCRASESDVSYGHSFMQWYQKPGQPKLLIYRASNLMP 60
DB 138 DIETQSPASLAVSLGQRATISCRASESDVSYGHSFMQWYQKPGQPKLLIYRASNLMP 197
XX
QY 61 GIRARFSGSGSDFTLTINPVADVAITYCCQSNEDPFTFGSGYKLEIKR 112
DB 198 GIRARFSGSGSDFTLTINPVADVAITYCCQSNEDPFTFGAGTRLEIKR 249
XX
RESULT 2
AAU07480
ID AAU07480 standard; Protein; 112 AA.
XX
AC AAU07480;
XX
DT 24-OCT-2001 (first entry)
XX
DE Synthetic antibody scFv(F8) light chain variable region, VL-F8.
XX
KW VL-F8; scFv(F8); antimicrobial; antiviral; cytostatic;
KW immunomodulatory; antibody; gene therapy; HIV; light chain;
KW human immunodeficiency virus; tumour; metabolic disorder;
KW immune disorder; auto-immune disorder.
XX
OS Synthetic.
XX
PN WO200149713-A2.
XX
PD 12-JUL-2001.

XX
PF 29-DEC-2000; 2000WO-IT00554.
XX
PR 30-DEC-1999; 99IT-RM00803.
XX
PA (CNEI) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.
PA (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.
XX
PI Benvenuto E, Franconi R, Desiderio A, Tavladoraki P;
XX
DR WPI; 2001-502555/55.
DR N-PSDB; AAS11886.
XX
PT Peptides which are able to confer stability and solubility to an
PT antibody comprising these peptides, useful for treating pathologies
PT (e.g. tumour) associated with accumulation of a molecule inside or
PT outside a human, or animal cell -
XX
PS Claim 8; Page 69; 109pp; English.
XX
CC The invention relates to peptides which are able to confer stability and
CC solubility to an antibody comprising these peptides. The peptides
CC are especially H-FR1, H-FR2, H-FR3, HFR4, L-FR1, L-FR2, L-FR3 or L-FR4
CC present within a variable region of an antibody which makes the antibody
CC soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to
CC H-FR4 are present within the variable region of the heavy chain of an
CC antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order
CC (H-FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and
CC peptides having the sequences of L-FR1 to L-FR4 are present within
CC the variable region of the light chain of an antibody, covalently
CC linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(L-FR2)-(L-CDR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and
CC polynucleotides (e.g. by gene therapy) are useful for the manufacture
CC of a medicament for the treatment of pathologies associated with
CC accumulation of a molecule inside or outside a human, animal cell
CC or plant cell. The pathologies are infectious (e.g. viral infections such
CC as HIV, human immunodeficiency virus, infections), tumour, metabolic and
CC immune (especially auto-immune) pathologies. The present sequence
CC represents the synthetic antibody scFv(F8), light chain variable region,
CC VL-F8. This antibody is used as the basis for the design of the
CC peptides and antibody molecules of the invention.
XX
SQ Sequence 112 AA;
XX
Query Match 1 92.7%; Score 543; DB 22; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.3e-39;
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
XX
QY 1 DIETQSPASLAVSLGQRATISCRASESDVSYGHSFMQWYQKPGQPKLLIYRASNLMP 60
DB 1 DIETQSPASLAVSLGQRATISCRASESDVSYGHSFMQWYQKPGQPKLLIYRASNLMP 60
XX
QY 61 GIRARFSGSGSDFTLTINPVADVAITYCCQSNEDPFTFGSGYKLEIKR 112
DB 61 GIRARFSGSGSDFTLTINPVADVAITYCCQSNEDPFTFGAGTRLEIKR 112
XX
RESULT 3
AAU07516
ID AAU07516 standard; Peptide; 112 AA.
XX
AC AAU07516;
XX
DT 24-OCT-2001 (first entry)
XX
DE Antibody scFv8 light chain variable region.
XX
KW Antimicrobial; antiviral; cytostatic; immunomodulatory;
KW antibody; gene therapy; HIV; human immunodeficiency virus; tumour;
KW metabolic disorder; immune disorder; auto-immune disorder; lysosyme;
KW antibody light chain variable region; scFv8.
XX
OS Synthetic.

XX XX WO200149713-A2.
 XX PN
 XX 12-JUL-2001.
 XX PD
 XX 29-DEC-2000; 2000WO-IT00554.
 XX PF
 XX 30-DEC-1999; 99IT-RM00803.
 XX PR
 XX (C/NEN) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.
 XX PA (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.
 XX PI Benvenuto E, Franconi R, Desiderio A, Taviadoraki P;
 XX DR WPI: 2001-502555/55.
 XX PT Peptides which are able to confer stability and solubility to an
 PT antibody comprising these peptides, useful for treating pathologies
 PT (e.g. tumour) associated with accumulation of a molecule inside or
 PT outside a human, or animal cell -
 XX PS
 XX Disclosure: Fig 4; 109pp; English.
 XX PA The invention relates to peptides which are able to confer stability and
 CC solubility to an antibody comprising these peptides. The peptides
 CC are especially H-FR1, H-FR2, HF-R3, HFR4, L-FR1, L-FR2, L-FR3 or L-FR4
 CC present within a variable region of an antibody which makes the antibody
 CC soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to
 CC H-FR4 are present within the variable region of the heavy chain of an
 CC antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order
 CC (H-FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and
 CC peptides having the sequences of L-FR1 to L-FR4 are present within
 CC the variable region of the light chain of an antibody, covalently
 CC linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(L-
 CC (L-FR2)-(L-CDR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and
 CC polynucleotides (e.g. by gene therapy) are useful for the manufacture
 CC of a medicament for the treatment of pathologies associated with
 CC accumulation of a molecule inside or outside a human, animal cell
 CC or plant cell. The pathologies are infectious (e.g. viral infections such
 CC as HIV, human immunodeficiency virus, infections), tumour, metabolic and
 CC immune (especially auto-immune) pathologies. The present sequence
 CC represents the antibody scfv8 light chain variable region, used as
 CC a basis for making mutant antibodies.
 CC XX
 S0 Sequence 112 AA:
 Query Match 92.7%; Score 543; DB 22; Length 112;
 Best Local Similarity 93.8%; Pred. No. 1.3e-39;
 Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 DIETLOSPASLAVSLGQRTATISCRASESVDSYGHSPMOWYQKPGQPPRLLYRASNLKP 60
 Db 1 DIETLOSPASLAVSLGQRTATISCRASESVDSYGHSPMOWYQKPGQPPRLLYRALNLES 60
 Oy 61 GIPARFSSGSGTDFTLTINPEADVATYYCOQSNEDPFTFGSGTKLEIKR 112
 Db 61 GIPARFSSGSGRTDFTLTINPEADVATYYCOQSNEDPFTFGSGTKLEIKR 112
 RESULT 4
 AAU07497 standard; Protein: 252 AA.
 AC AAU07497;
 XX 24-OCT-2001 (first entry)
 DT Synthetic antibody scfv(f8).
 XX Antimicrobial; antiviral; cytostatic;
 XX Immunomodulatory; antibody; gene therapy; HIV; light chain;
 KW human immunodeficiency virus; tumour; metabolic disorder;
 KW immune disorder; auto-immune disorder; scfv(f8);

KW cucumber mosaic virus.
 XX Synthetic.
 OS Key
 XX FH Location/Qualifiers
 FT Protein 1..125
 FT /label= VH
 FT /note= "Heavy chain variable region"
 FT Peptide 126..140
 FT /label= Linker_peptide
 FT /note= "This peptide is specifically claimed in claim 17"
 FT Protein 141..252
 FT /label= VL
 FT /note= "Light chain variable region"
 XX WO200149713-A2.
 XX PN
 XX 12-JUL-2001.
 XX PD
 XX 29-DEC-2000; 2000WO-IT00554.
 XX PF
 XX 30-DEC-1999; 99IT-RM00803.
 XX PR
 XX (C/NEN) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.
 XX PA (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.
 XX PI Benvenuto E, Franconi R, Desiderio A, Taviadoraki P;
 XX DR WPI: 2001-502555/55.
 XX N-PSDB; AAS11887.
 XX PT Peptides which are able to confer stability and solubility to an
 PT antibody comprising these peptides, useful for treating pathologies
 PT (e.g. tumour) associated with accumulation of a molecule inside or
 PT outside a human, or animal cell -
 XX PS
 XX Example 1: Page 81; 109pp; English.
 XX PA The invention relates to peptides which are able to confer stability and
 CC solubility to an antibody comprising these peptides. The peptides
 CC are especially H-FR1, H-FR2, HF-R3, HFR4, L-FR1, L-FR2, L-FR3 or L-FR4
 CC present within a variable region of an antibody which makes the antibody
 CC soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to
 CC H-FR4 are present within the variable region of the heavy chain of an
 CC antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order
 CC (H-FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and
 CC peptides having the sequences of L-FR1 to L-FR4 are present within
 CC the variable region of the light chain of an antibody, covalently
 CC linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(L-
 CC (L-FR2)-(L-CDR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and
 CC polynucleotides (e.g. by gene therapy) are useful for the manufacture
 CC of a medicament for the treatment of pathologies associated with
 CC accumulation of a molecule inside or outside a human, animal cell
 CC or plant cell. The pathologies are infectious (e.g. viral infections such
 CC as HIV, human immunodeficiency virus, infections), tumour, metabolic and
 CC immune (especially auto-immune) pathologies. The present sequence
 CC represents the synthetic antibody scfv(f8) which is used as a basis
 CC for constructing synthetic antibodies incorporating the peptides of the
 CC invention.
 CC XX
 S0 Sequence 252 AA:
 Query Match 92.7%; Score 543; DB 22; Length 252;
 Best Local Similarity 93.8%; Pred. No. 3e-39;
 Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 DIETLOSPASLAVSLGQRTATISCRASESVDSYGHSPMOWYQKPGQPPRLLYRASNLKP 60
 Db 141 DIETLOSPASLAVSLGQRTATISCRASESVDSYGHSPMOWYQKPGQPPRLLYRALNLES 200
 Oy 61 GIPARFSSGSGTDFTLTINPEADVATYYCOQSNEDPFTFGSGTKLEIKR 112
 Db 201 GIPARFSSGSGRTDFTLTINPEADVATYYCOQSNEDPFTFGSGTKLEIKR 252

RESULT 5
AAR13089
ID AAR13089 standard; Protein; 112 AA.
XX
AC AAR13089;
XX
DT 01-OCT-1991 (first entry)
XX
DE Murine 1B4 light chain-2 variable region.
XX
KM Monoclonal antibody; complementarity determining region; CDR;
KM Integrin; hybridoma 1B4; protein REI; Gal/REI; Ig.
XX
PN EP438312-A.
PN EP440351-A.
XX
PD 24-JUL-1991.
XX
PF 17-JAN-1991; 91EP-0300367.
XX
PR 20-DEC-1990; 90US-0627421.
PR 19-JAN-1990; 90US-0467692.
XX
PA (MERI) MERCK & CO INC.
XX
PI Law MF, Mark GE, Schmidt JA, Singer II;
XX
DR WPI; 1991-216985/30.
DR N-PSDB; AAO12684.
XX
PT New recombinant immunoglobulin(s) reactive with leukocyte CD18
PT complementarity regions useful in treatment of inflammation
XX
PS Disclosure; Fig 25; 77pp; English.
XX
CC A recombinant human Ig comprises a human heavy chain framework
CC and murine CDRs (with the heavy chain framework mutated at sites
CC near the CDRs); a human light chain framework and murine CDRs.
CC It has a mean IC50 nearly equal to that of the murine monoclonal
CC antibody from which the CDRs were derived. It is designated
CC mutated Gal/REI. The human Ig is capable of binding to a human
CC CD18 integrin.
CC The murine CDRs are obtd. from murine hybridoma 1B4
CC (ATCC HB 10164). The light chain framework is derived from
CC human myeloma protein REI (EP-239400).
CC See also AAO12682-84.
XX
SQ Sequence 112 AA:
Query Match 92.2%; Score 540; DB 12; Length 112;
Best Local Similarity 92.9%; Pred. No. 2.4e-39;
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIETOSPASLAVSLGGRATISCRASESVDSYGHSPFQWYQKPGOPPKLLIYRASNLKP 60
DB 1 DIVLTGSPASLAVSLGGRATISCRASESVDSYGHSPFQWYQKPGOPPKLLIYRASNLKP 60
QY 61 GIPARFSGSGSGTFTLTINPVEADVAATYYCOQSNEDPFTFGSGTKLEIKR 112
DB 61 GIPARFSGSGSRDFTLTINPVEADVAATYYCOQSNEDPFTFGSGTKLEIKR 112
RESULT 6
AAB77332
ID AAB77332 standard; Protein; 112 AA.
XX
AC AAB77332;
XX
DT 17-JUN-2002 (first entry)
XX

DE Mouse 1B4 light chain variable region SEQ ID NO 37.
XX
KM Mouse; human; immunoglobulin; antigenicity; immunogenicity.
XX
OS Mus sp.
XX
PN US2002034765-A1.
XX
PD 21-MAR-2002.
XX
PF 16-MAR-2001; 2001US-0810502.
XX
PR 19-AUG-1993; 93US-0109187.
PR 01-MAR-1996; 96US-0609218.
PR 01-AUG-1997; 97US-0905280.
PR 17-MAY-1991; 91US-0702217.
XX
PA (MERI) MERCK & CO INC.
XX
PI Daugherty BL, Mark GE, Padlan EA;
XX
DR WPI; 2002-338924/37.
XX
PT Identifying and replacing immunoglobulin surface amino acid residues
PT useful for converting the antigenicity of a first mammalian species to
PT a second mammalian species
XX
PS Example 1; Fig 12; 36pp; English.
XX
CC The invention relates to identifying differences (1) in mammalian species
CC specific surface amino acid residues on an immunoglobulin which converts
CC the antigenicity of a first mammalian species to a second mammalian
CC species. The new method is used for identifying and replacing
CC immunoglobulin surface amino acid residues which converts the
CC antigenicity of a first mammalian species to that of a second mammalian
CC species. The method simultaneously reduces the immunogenicity and
CC strictly preserves ligand binding properties. The replacement of exterior
CC amino acid residues has no effect on the ligand binding properties but
CC greatly alters immunogenicity. The present sequence is that of a PCR
CC primer used in the construction of the "venered" 1B4 heavy and light
CC chain variable regions onto these variable regions. The human signal and
CC intronic sequences onto these variable regions. The present sequence is
CC that of the mouse 1B4 light chain variable region.
XX
SQ Sequence 112 AA:
Query Match 92.2%; Score 540; DB 23; Length 112;
Best Local Similarity 92.9%; Pred. No. 2.4e-39;
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIETOSPASLAVSLGGRATISCRASESVDSYGHSPFQWYQKPGOPPKLLIYRASNLKP 60
DB 1 DIVLTGSPASLAVSLGGRATISCRASESVDSYGHSPFQWYQKPGOPPKLLIYRASNLKP 60
QY 61 GIPARFSGSGSGTFTLTINPVEADVAATYYCOQSNEDPFTFGSGTKLEIKR 112
DB 61 GIPARFSGSGSRDFTLTINPVEADVAATYYCOQSNEDPFTFGSGTKLEIKR 112
RESULT 7
AAR47494
ID AAR47494 standard; Protein; 111 AA.
XX
AC AAR47494;
XX
DT 06-JUL-1994 (first entry)
XX
DE Murine anti-CD18 Ab 60.3 light chain.
XX
KM Monoclonal antibody; MAb; heavy chain; light chain;
KM constant region; variable region; amplification; primer;
KM polymerase chain reaction; PCR; chimera; Ig;
KM immunoglobulin; humanised antibody; leucocyte; integrin.
XX

XX	Mus sp.
XS	
XX	EP578515-A.
FN	
XX	12-JAN-1994.
PD	
XX	
PE	24-MAY-1993; 93EP-0401328.
XX	
PR	26-MAY-1992; 92US-0888233.
XX	
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	
PI	Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;
DR	WPI; 1994-010334/02.
NR	N-PSDB; AAO55002.
XX	
PT	Humanised monoclonal antibodies prepn. - using comparative model
XX	building, by computer database searching
XX	
PS	Disclosure: Page 21, 68pp; English.
XX	
CC	A humanised monoclonal antibody corresponding to the murine anti-CD18
CC	antibody 60.3 was prepared. The variable (V) region sequences from
CC	both the heavy (H) and light (L) chains were determined from cDNA
CC	(amplified by PCR) and spliced onto human constant (C) regions,
CC	resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
CC	expressed in tissue culture (Agt8.653 mouse myeloma cells, detected
CC	by ELISA), and examined in binding assays. The results from
CC	competition and inhibition assays showed that the chimeric Ab was
CC	as effective as the murine 60.3 Mab. The deduced murine VH and VL
CC	protein sequences were compared to the protein sequence data base,
CC	and two human Ig protein sequences were selected to be used as
CC	templates. A murine 60.3 Fv was modeled according to the deduced
CC	VH and VL protein sequences. Based on the 60.3 Fv model and the two
CC	human template sequences selected from the protein data base, a
CC	humanised Fv was modeled. Construction of the humanised 60.3 was
CC	done by plecting 5 pairs of complementary oligonucleotides together
CC	(spanning the entire V region) to form the VH and VL. These were
CC	then attached onto vectors containing genes for appropriate C regions
CC	to form humanised Ab (IgG1, kappa). The humanised proteins were again
CC	expressed in Agt8.653 cells and binding assays were done. FACS analyses
CC	indicated that the humanised Ab recognised cells expressing CD18.
CC	About a dozen of the humanised 60.3 Ab master wells were transferred
CC	and assayed for Ig.
XX	
SO	Sequence 111 AA;
	Query Match 91.0%; Score 533; DB 15; Length 111;
	Best Local Similarity 93.7%; Pred. No. 9.5e-39;
	Matches 104; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
OY	1 DIELQSPASLASLSGORRTICRSASESDSGHSFMOTYQKPPQPKLLIYRASNEP 60
Db	1 DIVLGSPASLAVALSAGORRTISCRASESDSGNSFMYHQKPPQPKLLIYRASNLE 60
OY	61 GIPIAFSSGSGCTDFTLTINPEADVDATYYCOQSNEDEPFGSGTKLEIK 111
Db	61 GIPIAFSSGSGRTDFTLTINPEADVDATYYCOQSNEDEPRTTGGTGKLEIK 111
RESULT 8	
ID	AAO01143
XX	AAO01143 standard; Protein: 131 AA.
AC	AAO01143;
XX	
DT	10-FEB-1997 (first entry)
XX	
DE	MAb 1.4 light chain, directed against type II phospholipase A2.
XX	
KW	Monoclonal antibody; phospholipase; myocardial infarction;

KW		pancreatitis; cerebral infarction; acute kidney failure; colitis;
KW		chronic rheumatism; adult respiratory distress syndrome;
KW		cardiac shock; treatment; preclinical testing; disease; hybridoma.
XX		
OS	Mus musculus.	
XX		
FH	Key	Location/Qualifiers
FT	Binding-site	44..58
FT	/label- CDR 1	
FT	Binding-site	74..80
FT	/label- CDR 2	
FT	Binding-site	113..121
FT	/label- CDR 3	
XX		
PN	WO9620959-A1.	
PD	11-JUL-1996.	
XX		
PF	27-DEC-1995;	95WO-JP02714.
XX		
PR	29-DEC-1994;	94JP-0340006.
XX		
PA	(YAMA) YAMANOCHI PHARM CO LTD.	
PI	Kawauchi Y, Masuko Y, Takasaki J, Yasunaga T;	
XX		
DR	WPI; 1996-333946/33.	
DR	N-PSDB; AAT40803.	
XX		
PT	Monoclonal antibody inhibiting type II phospholipase A2 activity	-
PT	for treatment of myocardial and cerebral infarction	
XX		
PS	Claim 6; Figure 10; 69pp; Japanese.	
XX		
CC	Monoclonal antibodies which inhibit type II phospholipase A2 are	
CC	useful in the treatment of myocardial infarction, cerebral	
CC	infarction, acute kidney failure, chronic rheumatism, cardiac shock,	
CC	pancreatitis, adult respiratory distress syndrome and colitis. The	
CC	antibodies were generated by immunising Balb/C mice with recombinant	
CC	human type II phospholipase A2. Splenic cells from the mice were	
CC	fused with mouse myeloma P3U1 (P3x63Ag8.U1) and the hybridomas	
CC	obtained were screened for phospholipase A2 inhibitory activity.	
CC	Active clones were isolated including 12H5, 1.4 and 10.1. These	
CC	were cultured and the antibody isolated from the culture	
CC	superantant by precipitation with ammonium sulphate and purification	
CC	on a column of protein A-Sepharose CL4B. Because the antibody acts	
CC	on the primate and mouse forms of enzyme as well as human it is	
CC	particularly suitable for preclinical testing.	
XX		
SQ	Sequence 131 AA:	
	Query Match 91.0%; Score 533; DB 17; Length 131;	
	Best Local Similarity 93.7%; Pred. No. 1.le-36;	
	Matches 104; Conservative 2; Mismatches 5; Indels 0; Gaps	0;
OY	1 DIETLOSPASLAVSLGQRATISCRASESVDSYGHSFMOMYOQKPGOPKLLIYRASNLEP 60	
Db	21 DVLVQGPSRLAVSLVGQRATISCRASESVDSYGHSFMHMYYOQKPGOPPRLILIRASNLES 80	
OY	61 GIPARFSGSGSTDFTLTINPEADVATYYCOQSNEPFTFGSGTKLEIK 111	
Db	81 GIPARFSGSGSTRFEFLTINPEADVATYYHCQSQSNEDEPFTFGSGTKLEIK 131	
RESULT 9		
AAM44168		
ID	AAM44168 standard; Protein; 131 AA.	
AC	AAM44168;	
XX		
DT	16-JUN-1998 (first entry)	
XX		
DE	Monoclonal antibody 1.4 light chain against type II phospholipase A2.	

XX Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin;
 KW amelioration; kidney disorder; nephrotoxicity; anticancer.
 XX Unidentified.
 OS WO9749427-A1.
 XX 31-DEC-1997.
 PD 27-JUN-1997; 97WO-JP02241.
 XX 19-SEP-1996; 96JP-0247635.
 PR 27-JUN-1996; 96JP-0167286.
 XX (YAMA) YAMANOUCHI PHARM CO LTD.
 PA Hayashi K, Kawachi Y, Masuno Y, Takasaki J;
 PI WPI: 1998-076914/07.
 DR N-PSDB: AAV12260.
 XX Amelioration of kidney disorders caused by cisplatin administration
 PT - by treatment with an antibody inhibiting type II phospholipase A2
 PT activity
 PS Disclosure: Page 35-36; 7app; Japanese.
 CC The present sequence represents the monoclonal antibody 1.4 light chain
 CC against type II phospholipase A2, from the present invention. The
 CC present invention describes a novel method for the amelioration of
 CC kidney disorders (such as acute renal failure) associated with the
 CC administration of cisplatin for the treatment of cancer. The method
 CC comprises treatment with a monoclonal antibody which inhibits the
 CC activity of type II phospholipase A2 (particularly of type II
 CC phospholipase A2 of human origin), or with a protein or peptide
 CC possessing the same inhibitory activity and containing a part of the
 CC antibody sequence. Preferably the antibody also inhibits the activity of
 CC ape and/or mouse type II phospholipase A2, and has the ability to
 CC release type II phospholipase A2 bound to a cell membrane. Three
 CC specific monoclonal antibodies having these properties which can be
 CC used are 12H5, 10.1 and 1.4, derived from hybridomas FERM BP-5300,
 CC FERM BP-5298 and FERM BP-5297 respectively. The method can be used for
 CC suppressing the nephrotoxicity which is a characteristic feature of
 CC cisplatin administration, and therefore allowing more efficient use of
 CC this drug as an anticancer agent, e.g. by allowing an increased dosage
 CC to be used.
 XX SQ Sequence 131 AA;
 Query Match 91.0%; Score 533; DB 19; Length 131;
 Best Local Similarity 93.7%; Pred. No. 1,1e-38;
 Matches 104; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 OY 1 DIETQSPSLAVSLGQRTATCRASESVSYGHSFMOWYQKPGQPKLLIYRASNEEP 60
 DB 21 DIVLQSPSLAVSLGQRTATCRASESVSYGHSFMOWYQKPGQPKLLIYRASNEES 80
 OY 61 GTPARSSGSGSTDTLTINPEVADVAATYYCOQSNEDPFTGSGKLEIK 111
 DB 81 GTPARSSGSGSTDTLTINPEVADVAATYYCOQSNEDPFTGSGKLEIK 131
 RESULT 10
 AAB20442 standard; Protein; 294 AA.
 XX AAB20442;
 AC 21-JUN-2001 (first entry)
 DT Anti-FIX/FIXa antibody 198/BI-myc-tag fusion.
 DE XX

KW Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
 KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
 KW myc-tag.
 XX Chimeric - Mus musculus.
 OS Chimeric - Synthetic.
 OS Chimeric - Escherichia coli.
 XX Key
 FT Location/Qualifiers
 FT 1..22
 FT /label= Signal_peptide
 FT 23..294
 FT /label= Mature_protein
 FT 23..271
 FT /label= scFv
 FT 23..144
 FT /label= VH
 FT /label= VL
 FT Misc-difference 76
 FT /note= "encoded by GGN"
 FT Peptide 145..159
 FT /label= Linker
 FT Region 160..271
 FT /label= VL
 FT Peptide 272..274
 FT /label= Spacer
 FT Protein 275..286
 FT /label= Myc_tag
 FT Peptide 287..288
 FT /label= Spacer
 FT Peptide 289..294
 FT /label= His_tag
 PN WO200119992-A2.
 XX 22-MAR-2001.
 PD 13-SEP-2000; 2000WO-EP08936.
 PF 14-SEP-1999; 99AT-0001576.
 PR (BAXT) BAXTER AG.
 PA Schefflinger F, Kerschbaumer R, Falkner F, Dorner F;
 DR WPI: 2001-290358/30.
 XX N-PSDB: AAF30732.
 XX New factor IX/factor IXa antibodies and their derivatives useful for
 PT increasing amidolytic activity of factor IXa, and for treating blood
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis
 XX Example 16; Fig 34; 138pp; English.
 XX The present sequence is that of a fusion protein comprising: a pelb
 CC leader; a single chain Fv (scFv) derivative of antibody 198/BI
 CC comprising the heavy (VH) and light (VL) chain variable regions of
 CC 198/BI joined by an artificial, flexible linker peptide; a spacer;
 CC a myc-tag peptide; a spacer; and a C-terminal 6His affinity tail.
 CC 198/BI is an example of anti-human factor IX (FIX)/activated factor
 CC IX (FIXa) antibodies of the invention. Anti-FIX/FIXa antibodies and
 CC their derivatives, including scFv fragments, have FVIIIa cofactor
 CC activity or FIXa activating activity. Administration leads to an
 CC increase in the procoagulant activity of FIXa, even in the presence
 CC of FVIIIa inhibitors. This allows for rapid blood coagulation even
 CC in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor
 CC patients. The antibodies and derivatives are used in a claimed
 CC pharmaceutical composition for treating patients with blood
 CC coagulation disorders, especially haemophilia A and haemorrhagic
 CC diathesis. The scFv-myc-tag fusion was expressed in E. coli. It
 CC exhibited FVIII-like activity.
 XX SQ Sequence 294 AA;

```

Query Match      90.3%; Score 529; DB 22; Length 294;
Best Local Similarity 91.1%; Pred. No. 5.6e-38;
Matches 102; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSFMQWYQOKPGOPKLLIYRASNLKP 60
   |||||||
Db 160 DIVLTQSPASLAVSLGQRTATISCRASESVDSYGHSFMQWYQOKPGOPKLLIYRASNLKP 219
   |||||||

QY 61 GIPARFSGSGSTDTFTLTINPEADVATYTCQOSNEDPFTFGSGTKLEIKR 112
   |||||||
Db 220 GIPARFSGSGSTDTFTLTINPEADVATYTCQOSNEDPFTFGSGTKLEIKR 271
   |||||||

RESULT 11
AAB20437
ID AAB20437 standard; Protein: 732 AA.
AC AAB20437;
XX
XX 21-JUN-2001 (first entry)
DE
DE Anti-FIX/FIXa antibody 198/BI-alkaline phosphatase fusion.
XX
XX Factor IX; FIX: Factor IXa; scFv; antibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KW alkaline phosphatase.
XX
XX Chimeric - Mus musculus.
OS Chimeric - Synthetic.
OS Chimeric - Escherichia coli.
XX
XX Key Location/Qualifiers
FH Peptide 1..22
FT /label= Signal_peptide
FT /label= 23..732
FT Protein /label= Mature_protein
FT /label= 23..271
FT /label= scFv
FT /label= 23..144
FT /label= VH
FT Misc-difference 76
FT /note= "encoded by GGN"
FT Peptide 145..159
FT /label= Linker
FT Region 160..271
FT /label= VL
FT Peptide 272..275
FT /label= Spacer
FT Protein 276..725
FT /label= Alkaline_phosphatase
FT Peptide 726..732
FT /label= His_tag

WO200119992-A2.
PD 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-EP08936.
XX
XX 14-SEP-1999; 99AT-0001576.
XX
XX (BAXT ) BAXTER AG.
XX
XX Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;
PI WPI: 2001-290358/30.
XX
XX N-PSDB: AAB30727.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis

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XX
XX Example 16: Fig 26; 138pp; English.
PS
XX The present sequence is that of a fusion protein comprising: a PelB
XX leader; a single chain Fv (scFv) derivative of antibody 198/BI
CC comprising the heavy (VH) and light (VL) chain variable regions of
CC 198/BI joined by an artificial, flexible linker peptide; a spacer;
CC Escherichia coli alkaline phosphatase; and a C-terminal 6His
CC affinity tag. 198/BI is an example of anti-human factor IX
CC (FIX)/activated factor IX (FIXa) antibodies of the invention.
CC Anti-FIX/FIXa antibodies and their derivatives, including scFv
CC fragments, have FVIIIa cofactor activity or FIXa activating
CC activity. Administration leads to an increase in the procoagulant
CC activity of FIXa, even in the presence of FVIIIa inhibitors. This
CC allows for rapid blood coagulation even in the absence of FVIII or
CC FVIIIa, and in the case of FVIII inhibitor patients. The
CC antibodies and derivatives are used in a claimed pharmaceutical
CC composition for treating patients with blood coagulation disorders,
CC especially haemophilia A and haemorrhagic diathesis. The
CC scFv-alkaline phosphatase was expressed in E. coli. It exhibited
CC FVIII-like activity.
XX
XX Sequence 732 AA:
SQ
XX
XX Query Match      90.3%; Score 529; DB 22; Length 732;
XX Best Local Similarity 91.1%; Pred. No. 1.4e-37;
XX Matches 102; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSFMQWYQOKPGOPKLLIYRASNLKP 60
   |||||||
Db 160 DIVLTQSPASLAVSLGQRTATISCRASESVDSYGHSFMQWYQOKPGOPKLLIYRASNLKP 219
   |||||||

QY 61 GIPARFSGSGSTDTFTLTINPEADVATYTCQOSNEDPFTFGSGTKLEIKR 112
   |||||||
Db 220 GIPARFSGSGSTDTFTLTINPEADVATYTCQOSNEDPFTFGSGTKLEIKR 271
   |||||||

RESULT 12
AAR29008
ID AAR29008 standard; Protein: 131 AA.
AC AAR29008;
XX
XX 30-MAR-1993 (first entry)
DE
DE p64-k4 protein product.
XX
XX Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
KW plasmid; p64-k4; p64-h2.
XX
XX Synthetic.
OS
OS Key Location/Qualifiers
FH Peptide 1..20
FT /note= "Signal peptide"
FT Protein 21..131
FT /note= "Mature peptide"

WO9219759-A.
PD 12-NOV-1992.
XX
XX 24-APR-1992; 92WO-JP00544.
XX
XX 25-APR-1991; 91JP-0095476.
XX
XX 19-FEB-1992; 92JP-0032084.
XX
XX (CHUS ) CHUGAI SETYAKU KK.
XX
XX Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
PI WPI: 1992-398882/48.
XX

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DR N-PSDB; AAQ30157.
 XX Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 XX
 PS Disclosure; Page 124-125; 207pp; Japanese.
 CC
 CC The sequences given in AAR29008-09 were encoded by plasmids which were
 CC used in example to illustrate the production of a human antibody which
 CC recognises human interleukin-6 receptor (IL-6R). The antibody
 CC comprises light (L) chain and heavy (H) chain variable regions which
 CC were derived from a mouse monoclonal antibody produced from the
 CC hybridoma AUK64-7 which contained the plasmids p64-K4 and p64-h2.
 XX
 SQ Sequence 131 AA;
 Query Match 89.6%; Score 525; DB 13; Length 131;
 Best Local Similarity 91.9%; Pred. No. 5.5e-38;
 Matches 102; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DIETQSPASISLQGRATISCRASESDYSGHSFQMOWQKPGQPKLLIRASMLEP 60
 DB 21 DIVLTQSPASISLQGRATISCRASESDYSGHSFQMOWQKPGQPKLLIRASMLE 80
 QY 61 GIPARFSGSGSTFTLTINPEADVAITYCCQSNEDPFTFGSGTKLEIK 111
 DB 81 GIPARFSGSGSTFTLTINPEADVAITYCCQSNEDPFTFGAGTKLEIK 131
 RESULT 13
 AAB20438
 ID AAB20438 standard; Protein; 325 AA.
 XX
 AC AAB20438;
 XX
 DT 21-JUN-2001 (first entry)
 XX
 DE Anti-Fix/Fixa antibody 198/B1 bivalent miniantibody.
 XX
 XX Factor IX; FIX; Factor IXa; Fixa; miniantibody; procoagulant;
 KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 KW haemorrhagic diathesis; haemostatic; amido-lytic; therapy; mouse;
 KW bivalent antibody; plasmid p2ip-198AB2#102.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Synthetic.
 OS Chimeric - Escherichia coli.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /label= Signal_peptide
 FT /note= "Peib leader"
 FT Protein 23..325
 FT /label= Mature_protein
 FT Protein 23..271
 FT /label= scfv
 FT Region 23..144
 FT /label= VH
 FT Misc-difference 76
 FT /note= "encoded by GGN"
 FT Peptide 145..159
 FT /label= Linker
 FT Region 160..271
 FT /label= VL
 FT Misc-difference 166
 FT /note= "encoded by TNM"
 FT Misc-difference 181
 FT /note= "encoded by TCN"
 FT Peptide 272..274
 FT /label= Spacer
 FT Protein 275..284
 FT /label= Hinge

FT Protein 285..319
 FT /label= Helix
 FT Peptide 320..325
 FT /label= His_tag
 XX
 PN WO200119992-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 13-SEP-2000; 2000MO-EP08936.
 XX
 PR 14-SEP-1999; 99AT-0001576.
 XX
 PA (BAXT) BAXTER AG.
 XX
 PI Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;
 DR WPI; 2001-290358/30.
 DR N-PSDB; AAF30728.
 XX
 PT New factor IX/factor IXa antibodies and their derivatives useful for
 PT increasing amidolytic activity of factor IXa, and for treating blood
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis
 XX
 PS Example 16; Fig 28; 138pp; English.
 XX
 CC The present sequence is that of a bivalent miniantibody comprising
 CC a Peib leader peptide, the single chain Fv (scfv) fragment of
 CC antibody 198/B1 (subclone AB2), an amphipathic helical structure
 CC and a C-terminal 6His tag. The protein was expressed in
 CC Escherichia coli from plasmid p2ip198AB2#102 (see AAF30728).
 CC Antibody 198/B1 is an example of anti-human Factor IX
 CC (FIX)/activated Factor IX (FIXa) antibodies of the invention.
 CC Anti-Fix/Fixa antibodies and their derivatives have FVIII cofactor
 CC activity or FIXa activating activity. Administration leads to an
 CC increase in the procoagulant activity of FIXa, even in the presence
 CC of FVIII inhibitors. This allows for rapid blood coagulation even
 CC in the absence of FVIII or FVIIIa, and in the case of FVIII
 CC inhibitor patients. The antibodies and derivatives are used in a
 CC claimed pharmaceutical composition for treating patients with blood
 CC coagulation disorders, especially haemophilia A and haemorrhagic
 CC diathesis. The bivalent miniantibody exhibited FVIII-like
 CC activity.
 XX
 SQ Sequence 325 AA;
 Query Match 89.6%; Score 525; DB 22; Length 325;
 Best Local Similarity 90.2%; Pred. No. 1.4e-37;
 Matches 101; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 1 DIETQSPASISLQGRATISCRASESDYSGHSFQMOWQKPGQPKLLIRASMLEP 60
 DB 160 DIVLTQSPASISLQGRATISCRASESDYSGHSFQMOWQKPGQPKLLIRASMLE 219
 QY 61 GIPARFSGSGSTFTLTINPEADVAITYCCQSNEDPFTFGSGTKLEIK 112
 DB 220 GIPARFSGSGSTFTLTINPEADVAITYCCQSNEDPFTFGTKLEIK 271
 RESULT 14
 AAW30278
 ID AAW30278 standard; Protein; 131 AA.
 XX
 AC AAW30278;
 XX
 DT 07-JUL-1998 (first entry)
 XX
 DE Light chain of MUM4TS.11.
 XX
 XX MUM4TS.11; antibody; platelet; beta receptor; PDGF-R beta; inhibition;
 KW internal hyperplasia; vasculature; restenosis; angioplasty; light chain.
 XX
 OS Mus sp.

```

XX Key Location/Qualifiers
FH Protein 20..131
FT /note= "Mature protein"
FT Binding-site 43..58
FT /note= "Complementarity determining region 1"
FT Binding-site 73..80
FT /note= "Complementarity determining region 2"
FT Binding-site 112..120
FT /note= "Complementarity determining region 3"
XX
XX WO9737029-A1.
XX
XX 09-OCT-1997.
XX
XX 19-MAR-1997; 97WO-US04198.
XX
XX 22-MAR-1996; 96US-0621751.
XX
XX (BOE ) BOEHRINGER MANNHEIM GMBH.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Chang CN, Landolfi NF, Martin U;
XX
XX MPI; 1997-503114/46.
XX N-PSDB; AAT90985.
XX
XX Antibodies to platelet derived growth factor beta receptor - inhibit
XX PDGF BB-induced proliferation of cells expressing the receptor, used
XX particularly for inhibiting intimal hyperplasia
XX
XX Claim 11; Fig 7B; 87pp; English.
XX
XX This is the amino acid sequence for the light chain of muM4TS.11, a
XX novel antibody which specifically binds to the platelet derived
XX growth beta receptor (PDGF-R beta), but not within the fifth
XX extracellular Ig-like domain, where the antibody inhibits PDGF
XX BB-induced proliferation of a cell expressing the PDGF beta receptor.
XX The antibody can be used in a method of inhibiting intimal hyperplasia
XX in the vasculature of a mammal. The antibodies can be used for the
XX treatment of disorders related to PDGF activity such as disorders
XX involving proliferation of smooth muscle cells, and including
XX restenosis following angioplasty.
XX
XX Sequence 131 AA:
SQ
XX
XX Query Match 89.2%; Score 523; DB 18; Length 131;
XX Best Local Similarity 91.9%; Pred. No. 8.2e-38;
XX Matches 102; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 1 DIELTQSPASLAVSLGQRATISCRASESVDSYGHSMQYQKPGQPKLLIYRASNLDP 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX DB 21 DVLVQSPSLAVSLGQRATISCRASESVDSYGHSMQYQKPGQPKLLIYRASNLDP 80
XX
XX QY 61 GIPARFSGSGGSDFTLTINPVEADVDVATYYCOQSNEDPFTFGSGTKLEIKR 111
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX DB 81 GIPARFSGSGGSDFTLTINPVEADVDVATYYCOQSNEDPFTFGSGTKLEIKR 131
XX
XX RESULT 15
XX AAM02292
XX ID AAM02292 standard: Protein; 149 AA.
XX
XX AAM02292;
XX
XX 22-NOV-1996 (first entry)
XX
XX FVKC-II VL region.
XX
XX Single chain antibody; Fv; FVKC; heavy chain; light chain;
XX antibody engineering; peptide hormone; Pichia pastoris.
XX
XX Mus musculus.

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XX Key Location/Qualifiers
FH Peptide 1..22
FT /label= Pe1B_leader
FT Protein 23..136
FT /label= VLKC
FT Peptide 137..149
FT /label= HydropH11-II
FT /note= "HydropH11 II tag used to facilitate assay of Fv activity"
XX
XX WO9627612-A1.
XX
XX 12-SEP-1996.
XX
XX 01-MAR-1996; 96WO-GB00468.
XX
XX 03-MAR-1995; 95GB-0004344.
XX
XX (UNIL ) QUEST INT BV.
XX
XX Berry MJ, Davis PJ, Van Der Logt CPE, Whitejam GC;
XX
XX MPI; 1996-425380/42.
XX N-PSDB; AAT36906.
XX
XX Prodn. of antibody fragments, partic. in yeast - by prodn. of heavy
XX and light chains linked by sequence cleavable by host enzyme
XX
XX Disclosure; Fig 8; 53pp; English.
XX
XX FVKC VH (AAM02291) and VL (AAM02292) chains are encoded by a DNA
XX construct (AAT36906) assembled in E. coli vector pUC19. FVKC
XX is a single-chain antibody that shows specificity for a peptide
XX hormone. Novel antibody fragments (see also AAM02293-94) have
XX been constructed in which the FVKC VH and VL chains are separated
XX by a KEX2-type processing sites, allowing prodn. in yeast, partic.
XX Pichia pastoris, host cells.
XX
XX Sequence 149 AA:
SQ
XX
XX Query Match 89.1%; Score 522; DB 17; Length 149;
XX Best Local Similarity 90.4%; Pred. No. 1.1e-37;
XX Matches 103; Conservative 4; Mismatches 5; Indels 2; Gaps 1;
XX
XX QY 1 DIELTQSPASLAVSLGQRATISCRASESVDSYGHSMQYQKPGQPKLLIYRASNLDP 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX DB 23 DIELTQSPSLAVSLGQRATISCRASESVDSYGHSMQYQKPGQPKLLIYRASNLDP 82
XX
XX QY 61 GIPARFSGSGGSDFTLTINPVEADVDVATYYCOQSNEDP--FTFGSGTKLEIKR 112
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX DB 83 GIPARFSGSGGSDFTLTINPVEADVDVATYYCOQSNEDPYMYTFGGGTKLEIKR 136
XX
XX Search completed: January 13, 2003, 15:11:18
XX Job time : 31.1913 secs

```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:09:39 ; Search time 25.6522 Seconds
(without alignments)
947.817 Million cell updates/sec

Title:	US-09-144-886-63
Perfect score:	633
Sequence:	1 QVQLQESGGGLYKPGSLK.....YRDDAMDYWGQGTITVSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters:  671580
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
SPRSEMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*
```

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query length	DB	ID	Description
1	532	84.0	487	11	099K4	099K4 mus musculus
2	515.5	81.9	119	11	0920E7	0920E7 mus musculus
3	471	74.4	473	11	091205	091205 mus musculus
4	455.5	72.0	486	11	091207	091207 mus musculus
5	449.5	71.0	480	11	091X61	091X61 mus musculus
6	446.5	70.5	479	11	091WP5	091WP5 mus musculus
7	442	69.8	471	11	08RC77	08RC77 homo sapien
8	433	68.4	437	11	09RI4	09RI4 mus musculus
9	431	68.1	112	4	09HC1	09HC1 homo sapien
10	430.5	68.0	113	4	09UL90	09UL90 homo sapien
11	430	67.9	118	4	09UL91	09UL91 homo sapien
12	429.5	67.9	121	4	09UL71	09UL71 homo sapien
13	427	67.5	613	4	08WU1	08WU1 homo sapien
14	425	67.1	404	4	09EK68	09EK68 homo sapien
15	424.5	67.1	597	4	09EB89	09EB89 homo sapien
16	424	67.0	573	4	08WU38	08WU38 homo sapien

ALIGNMENTS

17	421	66.5	118	4	09UL72	09UL12	homo sapien
18	420.5	66.4	116	4	09UL93	09UL13	homo sapien
19	407	64.3	147	4	09Y509	09Y509	homo sapien
20	406	64.1	298	11	09QYF0	09QYF0	mus musculus
21	402	63.5	122	4	09UL84	09UL14	homo sapien
22	394	62.2	95	4	09UL86	09UL16	homo sapien
23	385	60.8	469	11	08RV9	08RV9	mus musculus
24	380.5	60.1	131	4	09UL88	09UL18	homo sapien
25	366	57.8	484	11	08VEA0	08VEA0	mus musculus
26	357	56.4	143	11	09ZAP9	09ZAP9	mus musculus
27	355	56.1	145	11	09ZAR4	09ZAR4	mus musculus
28	353.5	55.8	473	11	09DBL4	09DBL4	mus musculus
29	352.5	55.7	117	11	09QXE9	09QXE9	mus musculus
30	352	55.6	143	11	09ZAR0	09ZAR0	mus musculus
31	347	54.8	124	4	09UL92	09UL12	homo sapien
32	346.5	54.7	146	11	09ZQ03	09ZQ03	mus musculus
33	342	54.0	145	11	09ZAR1	09ZAR1	mus musculus
34	342	54.0	145	11	09ZQ07	09ZQ07	mus musculus
35	341.5	53.9	142	11	09ZQ01	09ZQ01	mus musculus
36	340.5	53.8	142	11	09ZQ02	09ZQ02	mus musculus
37	338.5	53.5	117	11	09QXF0	09QXF0	mus musculus
38	336.5	53.2	143	11	09ZAR8	09ZAR8	mus musculus
39	336	53.1	146	11	09ZAP6	09ZAP6	mus musculus
40	335	52.9	145	11	09ZQ06	09ZQ06	mus musculus
41	334.5	52.8	119	4	09UL87	09UL17	homo sapien
42	334.5	52.8	109	5	09GYZ2	09GYZ2	schistosoma
43	333	52.6	145	11	09ZAR0	09ZAR0	mus musculus
44	332	52.4	137	11	09ZAR6	09ZAR6	mus musculus
45	331.5	52.4	468	11	09UL31	09UL31	mus musculus

RESULT 1

ID	009K44	PRELIMINARY:	PRT:	487 AA.
AC	009K44:			
DT	01-JUN-2001 (TEMBLrel. 17, Created)			
DT	01-JUN-2001 (TEMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TEMBLrel. 19, Last annotation update)			
DE	Hypothetical 52.6 kDa protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
NP	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (MAR-2001) to the EMBL/genbank/DBJ databases.			
DR	EMBL: BC004786; AAH04786.1; -.			
DR	HSSP: P01810; 2EBJ.			
DR	InterPro: IPR003599; Ig.			
DR	InterPro: IPR003597; Ig-cl.			
DR	InterPro: IPR003600; Ig-like.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig-V.			
DR	Pfam: PF00047; Ig; 4.			
DR	SMART: SM00409; IG; 3.			
DR	SMART: SM00407; IGcl; 3.			
DR	SMART: SM00406; IGY; 1.			
DR	SMART: SM00410; IG_Like; 1.			
DR	PROSITE: PS00290; IG_MHC; UNKNOWN_2.			
DR	Hypothetical protein.			
KW	SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;			
QO				

Query Match:	84.0%	Score 537, DB 11	Length 487,
Best Local Similarity:	83.1%	Pred No. 7, 5e-45;	
Matches 103; Conservative	4;	Mismatches 11;	Indels 6; Gaps 1

Oy	1	QVQLQESGGGLVFRPGSKLTKSCA	SPTISDYMYWVRDTPKRL	EWVAISDG	SYTY	60
	:	---	---	---	---	
20	EVQLVEGGGLVFRPGSKLTKSCA	SPTISDYMYWVRDTPKRL	EWVAISDG	SYTY	79	

KW	Hypothetical protein.
SQ	SEQUENCE 473 AA; 51946 MW; CF625F008932AFL2 CXC64;
	Query Match 74.4%; Score 471; DB 11; Length 473;
	Best Local Similarity 75.4%; Pred. No. 8.8e-39;
	Matches 89; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
OY	1 QVOLESGGGLVKKPGGSILKLSCAASGFTEFSDDYMWVRQTPEKRLEWATISDGGSYYX 60
DB	EVLHVESGGGLVKPPGSKRLSCAAGTFPSSDGMHWRAQAPKGLEWAAYINSGSTTIYY 79
	: : : : : : : : : : :
OY	61 PDSVKGRTTISRDNKNNLTYLOMSSLKSSEDPTAMYCRRYRDAMDYWGQGTIVVSS 118
DB	ADTVAKGRITISDRNKNLTFLQMSTLRSDPDAMMYCARELMRLRIDYMGQGTIVVSS 137
	: : : : : : : : : : :
RESULT 4	
ID	Q91Z07 PRELIMINARY; PRT; 486 AA.
AC	Q91Z07;
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE	Hypothetical 52.7 kDa protein.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Strausberg R.;
RL	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC010324; AAB10324.1; -
DR	InterPro; IPR003598; IG_C2.
DR	InterPro; IPR003006; IG_MHC.
DR	Pfam; PF00047; Ig; 4.
DR	SMART; SM00408; IGC2; 1.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW	Hypothetical protein; Immunoglobulin domain.
SO	SEQUENCE 486 AA; 52682 MW; 4EEF83515DA870B CRC64;
	Query Match 72.0%; Score 455.5; DB 11; Length 486;
	Best Local Similarity 72.6%; Pred. No. 3.2e-37;
	Matches 90; Conservative 10; Mismatches 17; Indels 7; Gaps 3;
OY	1 QVOLESGGGLVKKPGGSILKLSCAASGFTEFSDDYMWVRQTPEKRLEWATISDGGSYYX 60
DB	EVLHVESGGGLVKPPGSKRLSCVVGFSFTSDMSVMWRTPERLREWWAATISGCGN-TYY 78
	: : : : : : : : : : :
OY	61 PDSVKGRTTISRDNKNNLTYLOMSSLKSSEDPTAMYCSR-----KYDDA-MHYMGQGTIV 114
DB	PDNVKGRFTVSRRDKAKYLTYLOMSSLKSSEDPAMYCVRPRIPIYYYSGSYFSDSMGQGTTI 138
	: : : : : : : : : : :
OY	115 TVSS 118
DB	139 TVSS 142
	: :
RESULT 5	
ID	Q91XE1 PRELIMINARY; PRT; 480 AA.
AC	Q91XE1;
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE	Unknown (Protein for IMAGE:4224494) (Fragment).
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Tissue-Colon;

RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010798; AAH10798.1; -
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER 1
SQ SEQUENCE 488 AA; 51936 MW; 120B9234EEF2B41ED CRC64;

Query Match 71.0%; Score 449.5; DB 11; Length 480;
Best Local Similarity 74.8%; Pred. No. 1.3e-36;
Matches 89; Conservative 11; Mismatches 14; Indels 5; Gaps 2;

OY 2 VOLQESGGGLVPGGSLKLSCAASGFTFSDDYMWVWROTPEKRLKLEWVATISDGSYTYYP 61
DB 20 VKLVSSGGGLVPGGSLKLSCAASGFTFSNYSWVWROTPEKRLKLEWVATISNGVATHTP 79
OY 62 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSR--YRYDAMDYWGCGTYYVSS 118
DB 80 DSMKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCTRGDYW--FDVWGAAGTYYVSS 135

RESULT 6
O91WP5 PRELIMINARY: PRT; 479 AA.
AC O91WP5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Hypothetical 51.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013656; AAH13656.1; -
DR InterPro: IPR003598; Ig_C2.
DR SMART: PF00047; Ig_4.
DR Pfam: SM00408; IGC2; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 70.5%; Score 446.5; DB 11; Length 479;
Best Local Similarity 73.7%; Pred. No. 2.5e-36;
Matches 87; Conservative 9; Mismatches 19; Indels 3; Gaps 1;

OY 1 OVQLOESGGGLVPGGSLKLSCAASGFTFSDDYMWVWROTPEKRLKLEWVATISDGSYTYYP 60
DB 20 EVQLVESGGGLVPGGSLKLSCAASGLTFSSYAMSWVWROTPEKRLKLEWVAINSNGNTYY 79
OY 61 PSDVKGRTISRDNKNNLYLQMSLSKSEDTAMYYCSRYYRYDAMDYWGCGTYYVSS 118
DB 80 SDTMKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCYVCRGY--FDVWGAAGTYYVSS 134

RESULT 7
O8TC77 PRELIMINARY: PRT; 471 AA.
AC O8TC77;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC024289; AAH24289.1; -
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF58660E CRC64;

Query Match 69.8%; Score 442; DB 4; Length 471;
Best Local Similarity 69.6%; Pred. No. 6.9e-36;
Matches 87; Conservative 12; Mismatches 16; Indels 10; Gaps 2;

OY 1 OVQLOESGGGLVPGGSLKLSCAASGFTFSDDYMWVWROTPEKRLKLEWVATISDGSYTYYP 60
DB 20 EVQLVESGGGLVPGGSLKLSCAASGFTFSYAMSWVWROTPEKRLKLEWVATISNGVATHTP 79
OY 61 PSDVKGRTISRDNKNNLYLQMSLSKSEDTAMYYCSR-----YRYDAMDYWGCGTYY 113
DB 80 ADSVKGRTISRDNKNNLYLQMSLSKSEDTAMYYCAR--GDYSAWGGTYYVSSA 136
OY 114 VTSS 118
DB 137 VTSS 141

RESULT 8
O9RI4 PRELIMINARY: PRT; 437 AA.
AC O9RI4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Gamma1 heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv)."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152372; AAD40243.1; -
DR HSP: P01842; 7FAB.
DR MGI: 96446; Igh-4.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IGLike; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 68.4%; Score 433; DB 11; Length 437;
Best Local Similarity 75.2%; Pred. No. 4.9e-35;
Matches 88; Conservative 6; Mismatches 19; Indels 4; Gaps 2;

OY 2 VOLQESGGGLVPGGSLKLSCAASGFTFSDDYMWVWROTPEKRLKLEWVATISDGSYTYYP 61
DB 1 VOLQESGGGLVPGGSLKLSCAASGFTFSYAMSWVWROTPEKRLKLEWVATISNGVATHTP 79
OY 62 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSRYYRYDAMDYWGCGTYYVSS 118
DB 60 DSVKGRFTISKDRNNILSLQMSLSKSEDTAMYYCAR--GDYSAWGGTYYVSSA 113

RESULT 9
09HCC1 PRELIMINARY; PRT; 112 AA.
ID 09HCC1
AC 09HCC1
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBL_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme: isolation from a
human synthetic phage display library and characterization."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -
DR HSSP; P01772; 2FB4.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24F1A5EC3B84788 CRC64;
Query Match 68.1%; Score 431; DB 4; Length 112;
Best Local Similarity 71.9%; Pred. No. 1.5e-35;
Matches 82; Conservative 14; Mismatches 16; Indels 2; Gaps 1;
QY 1 QVQLQESGGGLVPRGSGSLKSCAASGFTFSDDYMWYWRQTPERKLEWAVATISDGGSYTY 60
DB 1 EVQLVESGGGVPRGSGSLRISCAASGFTFPDQYMSVWRQAPGKLEWVSGINMGSGSTGY 60
QY 61 PDSYKGRFTISRDNKAKNNLYLQMSLSKSEPTAMYYCSRRYRDDAMDYWGCGTIVTS 114
DB 61 ADSYKGRFTISRDNKAKNNLYLQMSLSKSEPTAMYYCARRRY--ALDWYGGCTIV 112
RESULT 10
09UL90 PRELIMINARY; PRT; 113 AA.
ID 09UL90
AC 09UL90
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBL_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
CLin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -
DR HSSP; P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113

FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
Query Match 68.0%; Score 430.5; DB 4; Length 113;
Best Local Similarity 70.3%; Pred. No. 1.7e-35;
Matches 83; Conservative 14; Mismatches 16; Indels 5; Gaps 1;
QY 1 QVQLQESGGGLVPRGSGSLKSCAASGFTFSDDYMWYWRQTPERKLEWAVATISDGGSYTY 60
DB 1 EVQLVESGGGVPRGSGSLRISCAASGFTFSYGMHWWRQAPGKLEWVATIRYDSMKY 60
QY 61 PDSYKGRFTISRDNKAKNNLYLQMSLSKSEPTAMYYCSRRYRDDAMDYWGCGTIVTS 118
DB 61 ADSYKGRFTISRDNKAKNNLYLQMSLSKSEPTAMYYCARRRY--DLNWDGCTIVTSS 113
RESULT 11
09UL91 PRELIMINARY; PRT; 118 AA.
ID 09UL91
AC 09UL91
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBL_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
CLin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -
DR HSSP; P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;
Query Match 67.9%; Score 430; DB 4; Length 118;
Best Local Similarity 71.8%; Pred. No. 2e-35;
Matches 84; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
QY 1 QVQLQESGGGLVPRGSGSLKSCAASGFTFSDDYMWYWRQTPERKLEWAVATISDGGSYTY 60
DB 1 EVQLVESGGGVPRGSGSLRISCAASGFTFSYGMHWWRQAPGKLEWVATISSTIITTY 60
QY 61 PDSYKGRFTISRDNKAKNNLYLQMSLSKSEPTAMYYCSRRYRDDAMDYWGCGTIVTS 117
DB 61 ADSYKGRFTISRDNKAKNNLYLQMSLSKSEPTAMYYCARRRY--ALDWYGGCTIVTSS 117
RESULT 12
09UL71 PRELIMINARY; PRT; 121 AA.
ID 09UL71
AC 09UL71
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBL_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
CLin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -
DR HSSP; P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 121

[1]
SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035043; AAD56279.1; -.
DR HSSP: P01772; 12FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT 121 121
SO SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 67.9%; Score 429.5; DB 4; Length 121;
Best Local Similarity 67.8%; Pred. No. 2.3e-35;
Matches 82; Conservative 15; Mismatches 21; Indels 3; Gaps 1;

OY 1 QVOLOESGGGLVPGSGSLKSCASGFTFSDYYMWVROTPKRLKLEWVATISDGSSTYY 60
DB 1 EVOLVESGGGVYVPGSGSLKSCASGFTFSDYYMWVROAPGKLEWVATISDGSSTYY 60
OY 61 PDSVGRFTISDNKNNLYLQMSLSKSEDTAMYSKRYD---DAMDYGCCTTVYS 117
DB 61 ADSVGRFTISDNKNSLYLQMSLSRAEDTALYYCARGKVTIYDRDIMGCTMYVS 120
OY 118 S 118
DB 121 S 121

RESULT 13
O8WUK1 PRELIMINARY: PRT: 613 AA.
ID O8WUK1;
AC O8WUK1;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 67.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC020240; AAH20240.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00407; IGCL; 4.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein; Ig_MHC; UNKNOWN_3.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F950671E315 CRC64;

Query Match 67.5%; Score 427; DB 4; Length 613;
Best Local Similarity 70.0%; Pred. No. 3e-34;
Matches 84; Conservative 13; Mismatches 21; Indels 2; Gaps 1;

OY 1 QVOLOESGGGLVPGSGSLKSCASGFTFSDYYMWVROTPKRLKLEWVATISDGSSTYY 60
DB 20 QVOLOESGGGVYVPGSGSLKSCASGFTFSDYYMWVROAPGKLEWVATISDGSSTYY 79

OY 61 PDSVGRFTISDNKNNLYLQMSLSKSEDTAMYSKRYD---DAMDYGCCTTVYS 118
DB 80 ADSVGRFTISDNKNSLYLQMSLSRAEDTALYYCARGKVTIYDRDIMGCTMYVS 139

RESULT 14
O96K68 PRELIMINARY: PRT: 494 AA.
ID O96K68;
AC O96K68;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo
DE sapiens SNC73 protein (SNC73) mRNA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagaatsuma M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
RA Niinomiya K., Iwayanagi T.;
RT "NEBO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK027379; BAB55072.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SO SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AE4C0E CRC64;

Query Match 67.1%; Score 425; DB 4; Length 494;
Best Local Similarity 66.9%; Pred. No. 3.6e-34;
Matches 84; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

OY 1 QVOLOESGGGLVPGSGSLKSCASGFTFSDYYMWVROTPKRLKLEWVATISDGSSTYY 60
DB 20 EVOLVESGGGVYVPGSGSLKSCASGFTFSDYYMWVROAPGKLEWVATISDGSSTYY 79
OY 61 PDSVGRFTISDNKNNLYLQMSLSKSEDTAMYSKRYD---DAMDYGCCTTVYS 116
DB 80 PDSVGRFTISDNKNSLYLQMSLSRAEDTALYYCARGKVTIYDRDIMGCTMYVS 139
OY 117 S 118
DB 140 S 141

RESULT 15
O96BB9 PRELIMINARY: PRT: 597 AA.
ID O96BB9;
AC O96BB9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 65.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CELL;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015760; AAH15760.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 5.

DR	PROSITE; PS00230; IG_MHC.	UNKNOWN_3.
KM	Hypothetical protein.	
SO	SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;	

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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:10:24 : Search time 13.6348 Seconds
(without alignments)
789.676 Million cell updates/sec

Title: US-09-144-886-87

Perfect score: 586

Sequence: 1 DIETQSPASLAVSLGQRAT.....QQSNDEPFTGSGTKLEIKR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	539	92.0	111	1 KYMS37	Ig kappa chain V r
2	519	88.6	107	2 S26343	Ig kappa chain V r
3	515	87.9	115	2 S63596	Ig kappa chain V r
4	512	87.4	107	2 S26344	Ig kappa chain V r
5	512	87.4	131	1 KYMS6	Ig kappa chain pre
6	508	86.7	132	1 KYMS32	Ig kappa chain pre
7	500	85.3	111	2 S09965	Ig kappa chain V-J
8	498	85.0	111	1 KYMS43	Ig kappa chain V r
9	496	84.6	111	2 Da5722	Ig kappa chain V r
10	493	84.1	111	2 KYMS08	Ig kappa chain V r
11	487	83.1	111	1 KYMS83	Ig kappa chain V r
12	486	82.9	111	1 KYMS69	Ig kappa chain V r
13	482	82.3	111	2 E53285	Ig kappa chain V a
14	480	81.9	111	1 KYMSCL	Ig kappa chain V r
15	477	81.4	112	2 SI9972	Ig kappa chain V r
16	473	80.7	112	2 SI9971	Ig kappa chain V r
17	471	80.4	112	2 SI9976	Ig kappa chain V r
18	468.5	79.9	110	1 KYMS10	Ig kappa chain V r
19	468	79.9	131	2 PH1226	Ig kappa chain pre
20	467	79.7	111	1 KYMS75	Ig kappa chain V r
21	465	79.4	111	1 KYMS84	Ig kappa chain V r
22	465	79.4	111	1 KYMS40	Ig kappa chain V r
23	463	79.0	111	1 KYMS80	Ig kappa chain V r
24	462	78.8	210	2 A56169	Ig kappa chain V r
25	458	78.2	111	2 A33936	Ig kappa chain V r
26	457	78.0	111	2 S09969	Ig kappa chain V r
27	456	77.8	111	2 PI0081	Ig kappa chain V-J
28	456	77.8	112	2 S45715	Ig kappa chain V r
29	456	77.8	218	2 JC5810	monoclonal antibody

30	455	77.6	111	1 KYMS50	Ig kappa chain V r
31	455	77.6	111	1 KYMS85	Ig kappa chain V r
32	452	77.1	218	2 S68241	Ig kappa chain V r
33	449	76.6	111	2 S09966	Ig kappa chain V-J
34	447	76.3	111	2 S09963	Ig kappa chain V-J
35	447	76.3	131	2 S55027	Ig light chain pre
36	435.5	74.3	110	2 S24288	Ig kappa chain V r
37	434	74.1	109	2 PH0093	Ig kappa chain V r
38	434	74.1	111	2 S37202	Ig kappa chain V r
39	432	73.7	96	2 B49442	Ig kappa chain V r
40	427	72.9	108	1 KYMS54	Ig kappa chain V r
41	426	72.7	111	1 KYMS13	Ig kappa chain V r
42	426	72.7	140	2 PN0446	Ig kappa chain pre
43	420	71.7	120	2 S06731	Ig kappa chain pre
44	418	71.3	102	2 PH1079	Ig light chain V r
45	416.5	71.1	108	2 PH0092	Ig kappa chain V r

ALIGNMENTS

```
RESULT 1
KYMS37
Ig kappa chain V regions (PC3741, T111) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 21-Jan-2000
C:Accession: A93204; A93822; A01934
R:Weigert, M.; Gattalman, L.; Loh, E.; Schilling, J.; Hood, L.
N:ature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Contents: PC3741
A:Accession: A93204
A:Molecule type: protein
A:Residues: 1-111 <WEI>
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related
A:Reference number: A93822; MUID:79012520; PMID:99744
A:Contents: T111
A:Accession: A93822
A:Molecule type: protein
A:Residues: 1-111 <MCK>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match          92.0%; Score 539; DB 1; Length 111;
Best Local Similarity 93.7%; Pred. No. 6.8e-41;
Matches 104; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 DIETQSPASLAVSLGQRATISCRASESYDSYGHSPQWYQKPGQPKLLTYRASNLPP 60
DB 1 DIETQSPASLAVSLGQRATISCRASESYDSYGHSPQWYQKPGQPKLLTYRASNLPS 60
QY 61 GIPARESGSGRTDFTLTINPVADVDVATYYCOQSNDEPFTGSGTKLEIKR 111
DB 61 GIPARESGSGRTDFTLTINPVADVDVATYYCOQSNDEPFTGSGTKLEIKR 111

RESULT 2
S26343
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26343
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421; PMID:1908510
```


F:21-131/Domain: Ig kappa chain precursor V region #status experimental <MAT>
F:36-114/Domain: Immunoglobulin homology <IMM>
F:43-112/Disulfide bonds: #status predicted

Query Match 87.4% Score 512: DB 1: Length 131:
Best Local Similarity 88.3% Pred. No. 1.9e-38;
Matches 98: Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGQPPKLLIYRASNLDP 60
DB 21 NIVLTQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGQPPKLLIYRASNLDS 80

QY 61 GIPARFSGSGGTDFTLTINPEADVAITYCOQSNEDPFFGSGTKLEIK 111
DB 81 GIPARFSGSGGTDFTLTINPEADVAITYCOQSNEDPFFGSGTKLEIK 131

RESULT 6

KVMS32

Ig kappa chain precursor V regions (MOPC 321, TEPC 124) - mouse (tentative sequence)

C:Species: Mus musculus (house mouse)

C:Date: 31-May-1979 #sequence_revision 31-May-1979 #text_change 31-Mar-2000

C:Accession: A90412; A90373; A90374; A01933

R:Burstein, Y.; Schechter, I.

Biochemistry 17, 2392-2400, 1978

A:Title: Primary structures of N-terminal extra peptide segments linked to the variable expression of immunoglobulin genes.

A:Reference number: A90412; MUID:78235887; PMID:98179

A:Contents: MOPC 321

A:Accession: A90412

A:Molecule type: protein

A:Residues: 1-37 <BUR>

R:McKean, D.; Potter, M.; Hood, L.

Biochemistry 12, 749-759, 1973

A:Title: Mouse immunoglobulin chains. Partial amino acid sequence of a kappa chain.

A:Reference number: A90373; MUID:73140224; PMID:4120629

A:Contents: MOPC 321

A:Accession: A90373

A:Molecule type: protein

A:Residues: 21-132 <MCK>

A:Note: The partial sequence of the C region of this Bence Jones protein was also determined.

R:McKean, D.; Potter, M.; Hood, L.

Biochemistry 12, 760-771, 1973

A:Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains

A:Reference number: A90374; MUID:73140225; PMID:4651517

A:Contents: TEPC 124

A:Accession: A90374

A:Molecule type: protein

A:Residues: 21-131 <MC2>

A:Note: The sequence is compatible with that of MOPC 321 except in having 47-Glx, 51-Trp

C:Comment: The MOPC 321 sequence is shown.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 14

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-132/Product: Ig kappa chain V regions (MOPC 321, TEPC 124) #status predicted <MAT>

F:36-114/Domain: immunoglobulin homology <IMM>

F:43-112/Disulfide bonds: #status predicted

Query Match 86.7% Score 508: DB 1: Length 132:
Best Local Similarity 79.5% Pred. No. 4.4e-38;
Matches 99: Conservative 20; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGQPPKLLIYRASNLDP 60
DB 21 NIVLTQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGQPPKLLIYRASNLDS 80

QY 61 GIPARFSGSGGTDFTLTINPEADVAITYCOQSNEDPFFGSGTKLEIK 112
DB 81 GIPARFSGSGGTDFTLTINPEADVAITYCOQSNEDPFFGSGTKLEIK 132

RESULT 7

S09965

Ig kappa chain V-J region (106-10E) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000

C:Accession: S09965

R:Reininger, L.; Shiba, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.

Eur. J. Immunol. 20, 771-777, 1990

A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibody

A:Reference number: S09965; MUID:90269328; PMID:2347362

A:Accession: S09965

A:Molecule type: mRNA

A:Residues: 1-111 <RE>

A:Cross-references: EMBL:Z51853; NID:955394; PIDN:CAA83146.1; PID:9530230

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 85.3% Score 500: DB 2: Length 111:
Best Local Similarity 87.4% Pred. No. 1.9e-37;
Matches 97: Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGQPPKLLIYRASNLDP 60
DB 1 NIVLTQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGQPPKLLIYRASNLDS 60

QY 61 GIPARFSGSGGTDFTLTINPEADVAITYCOQSNEDPFFGSGTKLEIK 111
DB 61 GIPARFSGSGGTDFTLTINPEADVAITYCOQSNEDPFFGSGTKLEIK 111

RESULT 8

KVMS43

Ig kappa chain V region (PC7043) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000

C:Accession: A01937; S42187; S42190; S42189; S42188; S42191; S42192

R:Weigert, M.; Garmalan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: A01937

A:Molecule type: protein

A:Residues: 1-111 <WE>

R:Mo, J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42187

A:Molecule type: DNA

A:Residues: 12-99 <MO>

A:Cross-references: EMBL:Z25458; NID:9407844; PIDN:CAA80945.1; PID:9407845

A:Note: V-kappa-21E; anti-collagen

A:Accession: S42190

A:Molecule type: DNA

A:Residues: 13-99 <MO>

A:Cross-references: EMBL:Z25450; NID:9407838; PIDN:CAA80937.1; PID:9407839

A:Note: V-kappa-21E; anti-collagen

A:Accession: S42189

A:Molecule type: DNA

A:Residues: 15-99 <MO>

A:Cross-references: EMBL:Z25448; NID:9407836; PIDN:CAA80935.1; PID:9407837

A:Note: V-kappa-21E; anti-collagen

A:Accession: S42188

A:Molecule type: DNA

A:Residues: 12-99 <MO>

A:Cross-references: EMBL:Z25446; NID:9407834; PIDN:CAA80933.1; PID:9407835

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:08:33 : Search time 8.72174 Seconds
(without alignments)
561.150 Million cell updates/sec

Title: US-09-144-886-63

Perfect score: 633

Sequence: 1 OVQLQESGGGLVKGSLK.....YRYDAMDYWGCGITVTVSS 118

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	508	80.3	98	1 HV57_MOUSE	P18528 mus musculus
2	452	71.4	136	1 HV16_MOUSE	P01784 mus musculus
3	448	70.8	117	1 HV54_MOUSE	P18525 mus musculus
4	443	70.0	117	1 HV55_MOUSE	P18526 mus musculus
5	439	69.4	117	1 HV58_MOUSE	P18529 mus musculus
6	437.5	68.1	97	1 HV56_MOUSE	P18527 mus musculus
7	431	66.1	117	1 HV59_MOUSE	P18530 mus musculus
8	425	67.1	122	1 HV3G_HUMAN	P01768 homo sapien
9	419	66.2	117	1 HV53_MOUSE	P01762 homo sapien
10	413	65.2	122	1 HV3A_HUMAN	P01771 homo sapien
11	404.5	63.9	121	1 HV3J_HUMAN	P01772 homo sapien
12	403	63.7	126	1 HV3K_HUMAN	P01770 homo sapien
13	401	63.3	111	1 HV35_MOUSE	P01804 mus musculus
14	398	62.9	119	1 HV38_MOUSE	P01780 mus musculus
15	397	62.7	114	1 HV3B_HUMAN	P01763 homo sapien
16	396	62.6	119	1 HV37_MOUSE	P01807 mus musculus
17	396	62.6	119	1 HV4Q_MOUSE	P01810 mus musculus
18	395	62.4	116	1 HV3T_HUMAN	P01781 homo sapien
19	393.5	62.2	119	1 HV3I_HUMAN	P01780 mus musculus
20	392.5	62.0	113	1 HV30_MOUSE	P01799 mus musculus
21	392.5	62.0	115	1 HV32_MOUSE	P01801 mus musculus
22	390.5	61.7	118	1 HV39_MOUSE	P01809 mus musculus
23	390	61.6	117	1 HV3C_HUMAN	P01764 homo sapien
24	388	61.3	122	1 HV2Q_MOUSE	P01789 mus musculus
25	387.5	61.2	119	1 HV3L_HUMAN	P01767 homo sapien
26	386.5	61.1	115	1 HV3F_HUMAN	P01773 homo sapien
27	385.5	60.9	113	1 HV27_MOUSE	P01796 mus musculus
28	385.5	60.9	123	1 HV19_MOUSE	P01788 mus musculus
29	385	60.8	122	1 HV21_MOUSE	P01790 mus musculus
30	384.5	60.7	115	1 HV33_MOUSE	P01802 mus musculus
31	384	60.7	114	1 HV01_CANFA	P01784 canis fam11
32	383.5	60.6	117	1 HV41_MOUSE	P01811 mus musculus
33	383.5	60.6	123	1 HV22_MOUSE	P01791 mus musculus

34	382.5	60.4	113	1 HV31_MOUSE	P01800 mus musculus
35	382.5	60.4	123	1 HV25_MOUSE	P01794 mus musculus
36	381.5	60.3	116	1 HV05_CARAU	P19181 carassius a
37	381.5	60.3	123	1 HV18_MOUSE	P01787 mus musculus
38	381.5	60.3	123	1 HV23_MOUSE	P01792 mus musculus
39	381.5	60.3	123	1 HV24_MOUSE	P01793 mus musculus
40	381	60.2	113	1 HV3B_HUMAN	P01769 homo sapien
41	379.5	60.0	112	1 HV28_HUMAN	P01797 mus musculus
42	378.5	59.8	117	1 HV02_CANFA	P01785 canis fam11
43	378.5	59.8	144	1 HV26_MOUSE	P01795 mus musculus
44	376.5	59.5	142	1 HV01_RAT	P01805 ratius norv
45	375.5	59.3	113	1 HV29_MOUSE	P01798 mus musculus

ALIGNMENTS

RESULT 1

ID	Sequence	STANDARD	PRT	98 AA
AC	P18528;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V region 6.96.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	STRAIN-BALB/CJ;			
RX	MEDLINE=89279149; PubMed=2499654;			
RA	Levy N.S., Malpietro U.V., Lebecque S.G., Gearhart P.J.;			
RT	"Early onset of somatic mutation in immunoglobulin VH genes during			
RT	the primary immune response."			
RL	J. Exp. Med. 169:2007-2019(1989).			
CC	-1 MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.			
DR	PIR; J0501; HVMS96.			
DR	HSSP; P01772; 2FB4.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; ISG_1.			
KW	Immunoglobulin V region.			
FT	NON_TER			
SQ	SEQUENCE 98 AA; 11007 MW; B8644F7E92FBF95B CRC64;			
Query Match		80.3%;	Score 508; DB 1; Length 98;	
Best Local Similarity		96.9%;	Pred. No. 4.7e-45;	
Matches 95; Conservative		2; Mismatches 1; Indels	0; Gaps	0;
OY	1 OVQLQESGGGLVKGSLKSLKCAASGFTFSDDYMYVWRQTPKRLKLVATISDGSYTVY 60			
DB	1 EVQLVSGGGLVKGSLKSLKCAASGFTFSDDYMYVWRQTPKRLKLVATISDGSYTVY 60			
OY	61 PDSVKGRTISRDNKNNLYLQMSLSKSEDTATYCSR 98			
DB	61 PDSVKGRTISRDNKNNLYLQMSLSKSEDTATYCAR 98			
RESULT 2				
ID	HV16_MOUSE	STANDARD;	PRT;	136 AA.
AC	P01783;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V region MOPC 21 precursor (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=01234548; PubMed=6788376;
RA Rothwell A.L.M., Paskind M., Retz M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adeugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00522; AAD15290.1; -.
DR PIR: A02066; GIM52L.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90 DN -> DYAH (IN REF. 2).
FT CONFLICT 115 115 DN -> ND (IN REF. 2).
FT CONFLICT 120 120 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;

Query Match
Best Local Similarity 71.4%; Score 452; DB 1; Length 136;
Matches 90; Conservative 10; Mismatches 16; Indels 4; Gaps 2;

QY 2 VQLOESGGGLVPGGSLKSCAASGFTPSDYMYWVROTPERKLEWVATISDGGSTYY 61
DB 18 VQLVESGGGLVPGGSRKLSCAASGFTFSSFGMHVROAPEKLEWVATISSGSTLHYA 77
QY 62 DSVYGRFTISRDNKNNLYLQMSLSKSEDPAMYCSR---YRYDADNDYMGCTTVYSS 118
DB 78 DTVYGRFTISRDNKNNLYLQMTSLRSEDPAMYCARWGNPY-YAMDYGQGTSTVYSS 136

RESULT 3
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;

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RA Levy N.S., Malipiero U.V., Lebecqz S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J70505; HVMS84.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARTY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARTY-DETERMINING-2.
FT DISULFID 86 117 FRAMEWORK-3.
FT NON_TER 41 115 BY SIMILARITY.
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match
Best Local Similarity 70.8%; Score 448; DB 1; Length 117;
Matches 85; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVLOESGGGLVPGGSLKSCAASGFTPSDYMYWVROTPERKLEWVATISDGGSTYY 60
DB 20 EVKLVESGGGLVPGGSLKSCAASGFTFSSYMYWVROTPERKLEWVATISDGGSTYY 79
QY 61 PDSYGRFTISRDNKNNLYLQMSLSKSEDPAMYCSR 98
DB 80 PDSYGRFTISRDNKNNLYLQMSLSKSEDPAMYCAR 117

RESULT 4
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecqz S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J70502; HVMS34.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARTY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARTY-DETERMINING-2.
FT DISULFID 86 117 FRAMEWORK-3.
FT NON_TER 41 115 BY SIMILARITY.

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FT	DOMAIN	86	117	FRAMEWORK-3
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[illegible]

DE	Ig heavy chain V region RF precursor.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_Taxid=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-BALB/cJ;
KX	MEDLINE=89279149; PubMed=2496554;
RA	Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT	"Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";
RL	J. Exp. Med. 169:2007-2019(1989).
CC	-!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY. PIR: JTO503; HVMSRF.
DR	HSSP: P01810; ZEPJ.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	Pfam: PF00047; Ig_1.
DR	SMART: SM00406; Igv_1.
KW	Immunoglobulin V region; Hybridoma; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT	DOMAIN 20 49 FRAMEWORK-1.
FT	DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 55 68 FRAMEWORK-2.
FT	DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 86 117 FRAMEWORK-3.
FT	DISULFID 41 115 BY SIMILARITY.
FT	NON TER 117 117
SO	SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;
Query Match 66.2%; Score 419; DB 1; Length 117;	
Best Local Similarity 83.5%; Pred.No. 6.5e-36;	
Matches 81; Conservative 5; Mismatches 11; Indels 0; Gaps 0;	
Oy	2 VOLOSGGGGLKPPGSLKISCAASFTSDYYMYVWRQTPERKLFWATISDGSSTYP 61
Dy	21 VKLVSGGGGLVKLGSLKIKSCAASGFPTSSYSYMWVRQPERKLELVAAINSNGSTYP 80
Oy	62 DSVKGFTISRDNANKNYLQWSLSKSSEDTAMYYCSR 98
Dy	81 DTVGKFTISRDNANKNTLYLQWSLSKSSEDTALYYCAR 117
RESULT 10	
HV3A_HUMAN STANDARD: PRT: 122 AA.	
ID	HV3A_HUMAN
AC	P01762; 21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig heavy chain V-II region TRO.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE (MEYELMA PROTEIN TRO).
KX	MEDLINE=76023781; PubMed=809311;
RA	Kratzlin H., Altevogt P., Ruban E., Kort A., Starosck K., Hiltschmann N.;
RT	"The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), II. The amino acid sequence of the H-chain, alpha-type, subgroup III; structure of the complete IgA-molecule.";
RL	Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
CC	-!- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN. PIR: A02045; ALIHOTR.
DR	HSSP: P01772; ZFB4.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	Pfam: PF00047; Ig_1.
DR	SMART: SM00406; Igv_1.

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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:08:33 : Search time 8.27826 Seconds
(without alignments)
561.150 Million cell updates/sec

Title: US-09-144-886-87

Perfect score: 586

Sequence: 1 DIETLOSPASLAVSLGQRAT.....QQSNEDPFTFGSGTKLEIKR 112

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	539	92.0	111	KV3H_MOUSE	P01660 mus musculus
2	514	87.7	111	KV3J_MOUSE	P01662 mus musculus
3	512	87.4	131	KV3I_MOUSE	P01661 mus musculus
4	510	87.0	111	KV3K_MOUSE	P01663 mus musculus
5	508	86.7	132	KV3F_MOUSE	P01658 mus musculus
6	501	85.5	112	KV3G_MOUSE	P01659 mus musculus
7	498	85.0	111	KV3M_MOUSE	P01665 mus musculus
8	493	84.1	111	KV3O_MOUSE	P01667 mus musculus
9	487	83.1	111	KV3N_MOUSE	P01666 mus musculus
10	486	82.9	111	KV3Q_MOUSE	P01669 mus musculus
11	480	81.9	111	KV3L_MOUSE	P01664 mus musculus
12	468.5	79.9	110	KV3P_MOUSE	P01668 mus musculus
13	467	79.7	111	KV3S_MOUSE	P01671 mus musculus
14	465	79.4	111	KV3R_MOUSE	P01670 mus musculus
15	465	79.4	111	KV3T_MOUSE	P01672 mus musculus
16	463	79.0	111	KV3A_MOUSE	P01654 mus musculus
17	456.5	77.9	112	KV3B_MOUSE	P01655 mus musculus
18	455	77.6	111	KV3D_MOUSE	P01677 mus musculus
19	453	77.6	111	KV3U_MOUSE	P01673 mus musculus
20	454	77.5	111	KV3C_MOUSE	P01656 mus musculus
21	427	72.9	108	KV3V_MOUSE	P01674 mus musculus
22	426	72.7	111	KV3E_MOUSE	P01657 mus musculus
23	400	68.3	114	KV4A_HUMAN	P01625 homo sapien
24	399	68.1	108	KV5P_MOUSE	P01649 mus musculus
25	394	67.2	134	KV4C_HUMAN	P06313 homo sapien
26	387.5	66.1	133	KV4B_HUMAN	P06314 homo sapien
27	380	64.8	108	KV1M_HUMAN	P01605 homo sapien
28	376	64.2	108	KV1L_HUMAN	P01604 homo sapien
29	373.5	63.7	129	KV3M_HUMAN	P18136 homo sapien
30	373	63.7	108	KV1H_HUMAN	P01600 homo sapien
31	373	63.7	108	KV1N_HUMAN	P01606 homo sapien
32	371.5	63.4	129	KV1L_HUMAN	P18135 homo sapien
33	371	63.3	108	KV1Y_HUMAN	P80362 homo sapien

34	371	63.3	129	1	KV1M_HUMAN	P04431 homo sapien
35	370.5	63.2	109	1	KV3D_HUMAN	P01622 homo sapien
36	370	63.1	108	1	KV1E_HUMAN	P01594 homo sapien
37	370	63.1	108	1	KV1E_HUMAN	P01597 homo sapien
38	370	63.1	108	1	KV1F_HUMAN	P01607 homo sapien
39	370	63.1	108	1	KV1O_HUMAN	P01620 homo sapien
40	369.5	63.1	109	1	KV3B_HUMAN	P04207 homo sapien
41	368.5	62.9	129	1	KV3H_HUMAN	P01608 homo sapien
42	368	62.8	108	1	KV1P_HUMAN	P04430 homo sapien
43	368	62.8	108	1	KV1V_HUMAN	P01596 homo sapien
44	366.5	62.5	107	1	KV1D_HUMAN	P01603 homo sapien
45	365	62.3	108	1	KV1K_HUMAN	

ALIGNMENTS

RESULT 1	ID	Sequence	STANDARD:	PRT:	111 AA.
KV3H_MOUSE					
AC	P01660:	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-II region PC 3741/TEPC 111.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE (PC 3741).				
RA	MEDLINE=79073152; PubMed=103003;				
RT	Weigert M., Gattaman L., Loh E., Schilling J., Hood L.E.;				
RT	"Rearrangement of genetic information may produce Immunoglobulin				
RT	"diversity".				
RL	Nature 276:785-790(1978).				
RN	[2]				
RP	SEQUENCE (TEPC 111).				
RA	MEDLINE=79012520; PubMed=99744;				
RT	McKean D.J., Bell M., Potter M.;				
RT	"Mechanisms of antibody diversity: multiple genes encode structurally				
RT	related mouse kappa variable regions."				
CC	Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).				
DR	PIR; A01934; KVM37.				
DR	HSSP; P01679; 2F8U.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IGV_1.				
KW	Immunoglobulin V region.				
FT	DOMAIN 1..23				
FT	DOMAIN 24..38				
FT	DOMAIN 39..53				
FT	DOMAIN 54..60				
FT	DOMAIN 61..92				
FT	DOMAIN 93..101				
FT	DOMAIN 102..111				
FT	DISULFID 23..92				
FT	NON_TER 111				
SO	SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;				
Query Match	92.0%;				
Best Local Similarity	93.7%;				
Matches 104; Conservative	2; Mismatches 5; Indels 0; Gaps 0;				
Oy	1 DIETLOSPASLAVSLGQRATISCRASESDVSQSPWYQKPGQPKLLIYRASNLSP 60				
Db	1 DIETLOSPASLAVSLGQRATISCRASESDVSQSPWYQKPGQPKLLIYRASNLSP 60				
Oy	61 GIPARFSGSGSGTFTLTINPVADVDVATYYCOQSNEDPFTFGSGTKLEIK 111				
Db	61 GIPARFSGSGSGTFTLTINPVADVDVATYYCOQSNEDPFTFGSGTKLEIK 111				

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RESULT 2
KV3J_MOUSE STANDARD; PRT; 111 AA.
ID KV3J_MOUSE
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22);
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245);
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity."
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR HSP; A01935; KYMSM6.
DR HSP; P01679; 2FBU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_V.
DR SMART: SMO0406; IGV; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 53 FRAMEWORK-2.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 61 FRAMEWORK-3.
FT DOMAIN 6 92 FRAMEWORK-4.
FT DOMAIN 7 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 8 102 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SO SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 87.7%; Score 514; DB 1; Length 111;
Best Local Similarity 88.3%; Pred. No. 1,le-46;
Matches 98; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIETGSPASLAVSLGGRATISCRASVSVDYSGHSPQWYQKRGOPPKLLIYRASLTP 60
DB 1 NIYLTGSPASLAVSLGGRATISCRASVSVDYSGHSPQWYQKRGOPPKLLIYRASLTP 60
QY 61 GIPARFSGSGGTDFLTINPEADVATYCCQSNEDPFTFGSGTKLEIK 111
DB 61 GIPARFSGSGGTDFLTINPEADVATYCCQSNEDPFTFGSGTKLEIK 111

RESULT 3
KV3J_MOUSE STANDARD; PRT; 131 AA.
ID KV3J_MOUSE
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burslein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes."
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences."
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [4]
RP SEQUENCE.
RX HSP; A01935; KYMSM6.
DR HSP; P01679; 2FBU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_V.
DR SMART: SMO0406; IGV; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 1 21 43 FRAMEWORK-1.
FT DOMAIN 2 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 59 73 FRAMEWORK-2.
FT DOMAIN 4 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 81 112 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 6 113 121 FRAMEWORK-3.
FT DOMAIN 7 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
SO SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 87.4%; Score 512; DB 1; Length 131;
Best Local Similarity 88.3%; Pred. No. 2,2e-46;
Matches 98; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIETGSPASLAVSLGGRATISCRASVSVDYSGHSPQWYQKRGOPPKLLIYRASLTP 60
DB 21 NIYLTGSPASLAVSLGGRATISCRASVSVDYSGHSPQWYQKRGOPPKLLIYRASLTP 80
QY 61 GIPARFSGSGGTDFLTINPEADVATYCCQSNEDPFTFGSGTKLEIK 111
DB 81 GIPARFSGSGGTDFLTINPEADVATYCCQSNEDPFTFGSGTKLEIK 131

RESULT 4
KV3J_MOUSE STANDARD; PRT; 111 AA.
ID KV3J_MOUSE
AC P01663;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 kappa chain V-III region PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity."

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RL Nature 276:785-790(1978).
DR PIR: A01935; KWSM6.
DR HSSP: P01679; 2EBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 87.0%; Score 510; DB 1; Length 111;
Best Local Similarity 87.4%; Pred. No. 2.9e-46;
Matches 97; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSMQYQKPGQPKLLIYRASNLKP 60
DB 1 NIVLTQSPASLAVSLGQRTATISCRASESVDSYGHSMQYQKPGQPKLLIYRASNLKS 60

QY 61 GIPARFSGSGSTDEFTLTINPEADVDVATYYCQGSNEDPFTFGSGTKLEIKR 111
DB 61 GVPARFSGSGSRKTDFTLTIDPEADDAATYYCQGNEDPFTFGAGTKLEIK 111

RESULT 5
KV3F_MOUSE STANDARD; PRT; 132 AA.
ID KV3F_MOUSE
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MOPC 321 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=7823587; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-132.
RX MEDLINE=73140224; PubMed=4120629;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse Immunoglobulin chains. Partial amino acid sequence of a kappa
RT chain";
RL Biochemistry 12:749-759(1973).
CC -1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
CC REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
CC RESIDUES.
DR PIR: A01933; KWS32.
DR HSSP: P01679; 2EBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 132 IG KAPPA CHAIN V-II REGION MOPC 321.

FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 73 FRAMEWORK-2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 81 112 FRAMEWORK-3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BB73FBE9 CRC64;

Query Match 86.7%; Score 508; DB 1; Length 132;
Best Local Similarity 79.5%; Pred. No. 5.7e-45;
Matches 89; Conservative 20; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSMQYQKPGQPKLLIYRASNLKP 60
DB 21 DIVLTQSPASLAVSLGQRTATISCRASKSVNTYGNFMZYZZKPG2PPKLLIYRASNLKS 80

QY 61 GIPARFSGSGSTDEFTLTINPEADVDVATYYCQGSNEDPFTFGSGTKLEIKR 112
DB 81 GIPARFSGSGSRKTDFTLTIDPEADVDVATYYCQGSNEDPFTFGSGTKLEIKR 132

RESULT 6
KV3G_MOUSE STANDARD; PRT; 112 AA.
ID KV3G_MOUSE
AC P01659;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEPC 124.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse Immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences";
RL Biochemistry 12:760-771(1973).
DR PIR: A01933; KWS32.
DR HSSP: P01679; 2EBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12339 MW; 7CFD328DBE8E9D71 CRC64;

Query Match 85.5%; Score 501; DB 1; Length 112;
Best Local Similarity 79.5%; Pred. No. 2.5e-45;
Matches 89; Conservative 18; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSMQYQKPGQPKLLIYRASNLKP 60
DB 1 DIVLTQSPASLAVSLGQRTATISCRASZSVNMGNSFMZYZZKPG2PPKLLIYRASNLKS 60

QY 61 GIPARFSGSGSTDEFTLTINPEADVDVATYYCQGSNEDPFTFGSGTKLEIKR 112
DB 61 GIPARFSGSGSRKTDFTLTIDPEADVDVATYYCQGSNEDPFTFGSGTKLEIKR 112

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RESULT 7
KV3M_MOUSE
ID KV3M_MOUSE STANDARD: PRT: 111 AA.
AC P01665:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01937; KVM543.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
KW SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 FRAMEWORK-2.
FT DOMAIN 39 53 FRAMEWORK-3.
FT DOMAIN 54 60 FRAMEWORK-4.
FT DOMAIN 61 92 FRAMEWORK-5.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match
Best Local Similarity 85.0%; Score 498; DB 1; Length 111;
Matches 96; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

DYLTQSPASLAVSLGQRTATISCRASESYDSYGHSPQWYQKPGQPKLLITYASNLSP 60
DYLTPSPASLAVSLGQRTATISCRASESYDSYGHSPQWYQKPGQPKLLITYASNLSP 60
GTPARSSGSGGTFDTLTINPVADVDVATYYCOQSNEDPFTGSGTKLEIK 111
GTPARSSGSGGTFDTLTINPVADVDVATYYCOQSNEDPFTGSGTKLEIK 111
KV30_MOUSE
ID KV30_MOUSE STANDARD: PRT: 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: C01937; KVM508.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003006; Ig_MHC.

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DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 FRAMEWORK-2.
FT DOMAIN 39 53 FRAMEWORK-3.
FT DOMAIN 54 60 FRAMEWORK-4.
FT DOMAIN 61 92 FRAMEWORK-5.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4DC256D29 CRC64;

Query Match
Best Local Similarity 84.1%; Score 493; DB 1; Length 111;
Matches 95; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

DYLTQSPASLAVSLGQRTATISCRASESYDSYGHSPQWYQKPGQPKLLITYASNLSP 60
DYLTPSPASLAVSLGQRTATISCRASESYDSYGHSPQWYQKPGQPKLLITYASNLSP 60
GTPARSSGSGGTFDTLTINPVADVDVATYYCOQSNEDPFTGSGTKLEIK 111
GTPARSSGSGGTFDTLTINPVADVDVATYYCOQSNEDPFTGSGTKLEIK 111
KV3N_MOUSE
ID KV3N_MOUSE STANDARD: PRT: 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: B01937; KVM583.
DR HSSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
KW SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 FRAMEWORK-2.
FT DOMAIN 39 53 FRAMEWORK-3.
FT DOMAIN 54 60 FRAMEWORK-4.
FT DOMAIN 61 92 FRAMEWORK-5.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match
Best Local Similarity 83.1%; Score 487; DB 1; Length 111;
Matches 93; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

DYLTQSPASLAVSLGQRTATISCRASESYDSYGHSPQWYQKPGQPKLLITYASNLSP 60
DYLTPSPASLAVSLGQRTATISCRASESYDSYGHSPQWYQKPGQPKLLITYASNLSP 60

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OY 61 GIPARFSGSGSTDFLTINPVEADVAATYYCOQSNEDPFTGSGTKLEIK 111
 DB 61 GIPARFSGSGSTDFLTINHPVEEDAAATYYCOQSNEDPFTGAGTKLEIK 111

RESULT 10
 ID KV3Q_MOUSE STANDARD: PRT: 111 AA.

AC P01669: 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 7769.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: E01937; KVM569.
 DR HSSP: P80362; 1MTL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111
 SQ SEQUENCE 111 AA: 12011 MW: 6FAA345279356829 CRC64;

Query Match Best Local Similarity 82.9%; Score 486; DB 1; Length 111;
 Matches 93; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
 OY 1 DIETQSPASLAVSLGQRATISCRASESDSYGHSFMYOQKPGOPKLLIYRASNLSP 60
 DB 1 DIVLTQSPASLAVSLGQRATISCRASQSVYDGDSDYMNMYOQKPGOPKLLIYFASNLSP 60
 OY 61 GIPARFSGSGSTDFLTINPVEADVAATYYCOQSNEDPFTGSGTKLEIK 111
 DB 61 GIPARFSGSGSTDFLTINHPVEEDAAATYYCOQSNEDPFTGSGTKLEIK 111
 RESULT 11
 ID KV3L_MOUSE STANDARD: PRT: 111 AA.
 AC P01664: 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region CBPC 101.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 RT related mouse kappa variable regions.";

RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR: A01936; KVM5C1.
 DR HSSP: P80362; 1MTL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111
 SQ SEQUENCE 111 AA: 11964 MW: E2B1AD98AD965962 CRC64;

Query Match Best Local Similarity 81.9%; Score 480; DB 1; Length 111;
 Matches 92; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
 OY 1 DIETQSPASLAVSLGQRATISCRASESDSYGHSFMYOQKPGOPKLLIYRASNLSP 60
 DB 1 DIVLTQSPASLAVSLGQRATISCRASQSVYDGESIMNMYOQKPGOPKLLIYFASNLSP 60
 OY 61 GIPARFSGSGSTDFLTINPVEADVAATYYCOQSNEDPFTGSGTKLEIK 111
 DB 61 GIPARFSGSGSTDFLTINHPVEEDAAATYYCOQSNEDPFTGSGTKLEIK 111
 RESULT 12
 ID KV3P_MOUSE STANDARD: PRT: 110 AA.
 AC P01668: 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 7210.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: D01937; KVM510.
 DR HSSP: P01679; 2FBI.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 100
 FT DOMAIN 101 110
 FT DISULFID 23 92
 FT NON_TER 110
 SQ SEQUENCE 110 AA: 11950 MW: 69FLASCE86B1249 CRC64;

Query Match Best Local Similarity 79.9%; Score 468.5; DB 1; Length 110;
 Matches 92; Conservative 7; Mismatches 11; Indels 1; Gaps 1;
 OY 1 DIETQSPASLAVSLGQRATISCRASESDSYGHSFMYOQKPGOPKLLIYRASNLSP 60
 DB 1 DIVLTQSPASLAVSLGQRATISCRASQSVYDGDSDYMNMYOQKPGOPKLLIYFASNLSP 60
 OY 61 GIPARFSGSGSTDFLTINPVEADVAATYYCOQSNEDPFTGSGTKLEIK 111
 DB 61 GIPARFSGSGSTDFLTINHPVEEDAAATYYCOQSNEDPFTGSGTKLEIK 111
 RESULT 13
 ID KV3M_MOUSE STANDARD: PRT: 110 AA.
 AC P01669: 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 7210.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: D01937; KVM510.
 DR HSSP: P01679; 2FBI.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 100
 FT DOMAIN 101 110
 FT DISULFID 23 92
 FT NON_TER 110
 SQ SEQUENCE 110 AA: 11950 MW: 69FLASCE86B1249 CRC64;

OY 1 DIELTOSPASLAVSLGCRATISCRASESVDSYGHSMOWYQOKPGOPPKLLIYRASNLTP 60
 DB 1 DIELTOSPASLAVSLGCRATISCRASKASOSLDYDSDSYMMWYQOKPGOPPKLLIYRASNLTP 60
 OY 61 GIPARSSGSGGTDFLTINHPVADVATYCCOQSNEDPFTFGSGTKLEIK 111
 DB 61 GIPARSSGSGGTDFLTINHPVEEDATYCHOS-EDPWTFGSGTKLEIK 110
 RESULT 13
 KV3R_MOUSE
 ID KV3R_MOUSE STANDARD: PRT: 111 AA.
 AC P01671:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region PC 7175.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity";
 RL Nature 276:785-790(1978).
 DR PIR; B01938; KWS75.
 DR HSSP; P01679; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111
 SQ SEQUENCE 111 AA; 12010 MW; F041E99AA7858523 CRC64;
 Query Match 79.7%; Score 467; DB 1; Length 111;
 Best Local Similarity 80.2%; Pred. No. 8.4e-42;
 Matches 89; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
 OY 1 DIELTOSPASLAVSLGCRATISCRASESVDSYGHSMOWYQOKPGOPPKLLIYRASNLTP 60
 DB 1 DIELTOSPASLAVSLGCRATISCRASKASVSTSGSYMMWYQOKPGOPPKLLIYRASNLTP 60
 OY 61 GIPARSSGSGGTDFLTINHPVADVATYCCOQSNEDPFTFGSGTKLEIK 111
 DB 61 GIPARSSGSGGTDFLTINHPVEEDATYCHOSRELPLTFAGTKLEIK 111
 RESULT 14
 KV3R_MOUSE
 ID KV3R_MOUSE STANDARD: PRT: 111 AA.
 AC P01670:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region PC 6684.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity";
 RL Nature 276:785-790(1978).
 DR PIR; A01938; KWS84.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111
 SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;
 Query Match 79.4%; Score 465; DB 1; Length 111;
 Best Local Similarity 81.1%; Pred. No. 1.4e-41;
 Matches 90; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
 OY 1 DIELTOSPASLAVSLGCRATISCRASESVDSYGHSMOWYQOKPGOPPKLLIYRASNLTP 60
 DB 1 DIELTOSPASLAVSLGCRATISCRASKASVSTSGSYMMWYQOKPGOPPKLLIYRASNLTP 60
 OY 61 GIPARSSGSGGTDFLTINHPVADVATYCCOQSNEDPFTFGSGTKLEIK 111
 DB 61 GIPARSSGSGGTDFLTINHPVEEDATYCHOSRELPLTFAGTKLEIK 111
 RESULT 15
 KV3T_MOUSE
 ID KV3T_MOUSE STANDARD: PRT: 111 AA.
 AC P01672:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region PC 7940.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity";
 RL Nature 276:785-790(1978).
 DR PIR; C01938; KWS40.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111
 SQ SEQUENCE 111 AA; 12038 MW; EE8A82306084352E CRC64;

Query Match 79.4%; Score 465; DB 1; Length 111;
 Best Local Similarity 80.2%; Pred No. 1.4e-41;
 Matches 89; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

OY 1 DIELTQSPASLAVSLGQRTATISCRASESVDSYGHSPOMYQOKPGQPKLLIYRASNLSP 60
 |||||||||||||||||||:|:|:| ||||||||||| ||||
 Db 1 DIVLTQSPASLAVSLGQRTATISCRASKSVSAFGSYMHWYQOKPGQPKLLIYLASNLES 60
 |||||||||||||||||||:|:|:| ||||||||||| ||||

OY 61 GIPARFSGSGSGDTFTLTINPYEADDVATYYCOQSNEDPFTFGSGTKLEIK 111
 |:||||||||||||| |:|:| | ||| |||||
 Db 61 GVPARFSGSGSGDTFTLTINHPVEEDAVTYCOHSRELPPFTFGSGTKLEIK 111

Search completed: January 13, 2003, 15:11:39
 Job time : 8.27826 secs

